GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:49:49 ; Search time 23 Seconds
(without alignments)
1543.652 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 369
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	3.5	338	2	T41021	ser-thr protein ki
2	12	3.3	379	2	T23688	hypothetical prote
3	9	2.4	151	2	PC4223	rho kinase - pig (
4	9	2.4	251	2	G75345	serine/threonine-p
5	9	2.4	415	2	G01876	casein kinase I de
6	9	2.4	416	2	I61744	casein kinase I-ep
7	9	2.4	428	2	A46002	casein kinase I (E
8	9	2.4	546	2	AI2045	serine/threonine k
9	9	2.4	1173	2	T25539	hypothetical prote
10	9	2.4	1354	2	S74244	serine/threonine-s
11	9	2.4	1354	2	S69211	serine/threonine-s
12	9	2.4	1388	2	S70633	serine/threonine-s
13	9	2.4	1388	2	S74245	serine/threonine-s
14	8	2.2	258	2	H88130	protein F10G7.3 [i
15	8	2.2	282	2	D84375	ATP phosphoribosyl
16	8	2.2	351	2	T06749	hypothetical prote
17	8	2.2	363	2	T22107	hypothetical prote
18	8	2.2	393	2	A45176	protein kinase Dso
19	8	2.2	412	2	I78395	myotonic dystrophy
20	8	2.2	441	2	I78393	myotonic dystrophy
21	8	2.2	474	2	I78396	myotonic dystrophy
22	8	2.2	480	2	T47255	serine/threonine k
23	8	2.2	516	2	I78394	myotonic dystrophy
24	8	2.2	557	2	S71829	serine/threonine-s
25	8	2.2	562	2	A96713	hypothetical prote
26	8	2.2	598	2	T47254	serine/threonine k
27	8	2.2	605	2	S18648	protein kinase wis
28	8	2.2	614	2	F97381	hypothetical prote
29	8	2.2	614	2	AE2599	hypothetical prote
30	8	2.2	620	2	S22711	probable protein k
31	8	2.2	622	2	T10009	probable serine/th
32	8	2.2	622	2	H86910	probable serine/th
33	8	2.2	624	2	B49364	protein kinase (EC
34	8	2.2	626	1	D70699	probable pknB prot
35	8	2.2	665	2	S70706	probable protein k
36	8	2.2	668	2	S56909	polymyxin B resist
37	8	2.2	1548	2	T25808	hypothetical prote
38	7	1.9	126	2	S52255	copper resistance
39	7	1.9	128	1	NROW2	pancreatic ribonuc
40	7	1.9	149	2	S39910	S-receptor kinase
41	7	1.9	150	2	S31411	S-receptor kinase-
42	7	1.9	151	2	F98296	hypothetical prote
43	7	1.9	151	2	AB2987	hypothetical prote
44	7	1.9	154	2	T50898	hypothetical prote
45	7	1.9	162	2	S71633	MAP kinase kinase

ALIGNMENTS

RESULT 1
T41021
ser-thr protein kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41021
R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z21965
A;Accession: T41021
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-338 <MUR>
A;Cross-references: UNIPROT:O74426; UNIPARC:UPI0000069FF8; EMBL:AL023860; PIDN:CAA19590.1
A;Experimental source: strain 972h-; cosmid c162
C;Genetics:
A;Gene: SPDB:SPCC162.10
A;Map position: 3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 3.5%; Score 13; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         97 HRDVKPDNILLDE 109
              |||||||||||||
Db        149 HRDVKPDNILLDE 161
```

RESULT 2
T23688
hypothetical protein M03C11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23688
R;McMurray, A.
submitted to the EMBL Data Library, April 1995
A;Reference number: Z19783
A;Accession: T23688
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-379 <WIL>
A;Cross-references: UNIPROT:Q21483; UNIPARC:UPI000007B6C1; EMBL:Z49128; PIDN:CAA88953.1;
A;Experimental source: clone M03C11
C;Genetics:
A;Gene: CESP:M03C11.1
A;Map position: 3
A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 3.3%; Score 12; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 0.00088;

```
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 DLLLGGDLRYHL 65
              ||||||||||||
Db        106 DLLLGGDLRYHL 117


RESULT 3
PC4223
rho kinase - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Oct-2004
C;Accession: PC4223
R;Nishimura, J.; Sakihara, C.; Zhou, Y.; Kanaide, H.
Biochem. Biophys. Res. Commun. 227, 750-754, 1996
A;Title: Expression of rho A and rho kinase mRNAs in porcine vascular smooth muscle.
A;Reference number: PC4222; MUID:97040692; PMID:8886005
A;Accession: PC4223
A;Molecule type: mRNA
A;Residues: 1-151 <NIS>
A;Cross-references: UNIPROT:P79276; UNIPARC:UPI000017A471; DDBJ:D89493; NID:g1695732; PI
C;Comment: This enzyme mediates the inhibitor of myosin light chain.
F;1-151/Domain: protein kinase homology (fragment) <KIN>

  Query Match             2.4%;  Score 9;  DB 2;  Length 151;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         96 IHRDVKPDN 104
              |||||||||
Db         21 IHRDVKPDN 29


RESULT 4
G75345
serine/threonine-protein kinase-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75345
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75345
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-251 <WHI>
A;Cross-references: UNIPROT:Q9RTB4; UNIPARC:UPI00000D3EE4; GB:AE002025; GB:AE000513; NID
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1851
A;Map position: 1

  Query Match             2.4%;  Score 9;  DB 2;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. 0.68;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         97 HRDVKPDNI 105
              |||||||||
Db        128 HRDVKPDNI 136


RESULT 5
G01876
casein kinase I delta - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G01876
R;Kusuda, J.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08678
A;Accession: G01876
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-415 <KUS>
A;Cross-references: UNIPROT:P48730; UNIPARC:UPI0000153EE7; EMBL:U29171; NID:g881618; PID:
C;Superfamily: kinase-related transforming protein; protein kinase homology
F;7-279/Domain: protein kinase homology <KIN>

  Query Match             2.4%;  Score 9;  DB 2;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         96 IHRDVKPDN 104
              |||||||||
Db        125 IHRDVKPDN 133


RESULT 6
I61744
casein kinase I-epsilon - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I61744
R;Fish, K.J.; Cegielska, A.; Getman, M.E.; Landes, G.M.; Virshup, D.M.
J. Biol. Chem. 270, 14875-14883, 1995
A;Title: Isolation and characterization of human casein kinase I epsilon (CKI), a novel m
A;Reference number: A57011; MUID:95318039; PMID:7797465
A;Accession: I61744
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-416 <RES>
A;Cross-references: UNIPROT:P49674; UNIPARC:UPI000012DC67; GB:L37043; NID:g852056; PIDN:
C;Genetics:
A;Gene: GDB:CSNK1E; HCKIE
A;Cross-references: GDB:604574; OMIM:600863
A;Map position: 22q12-22q13
C;Superfamily: kinase-related transforming protein; protein kinase homology
F;7-279/Domain: protein kinase homology <KIN>

  Query Match             2.4%;  Score 9;  DB 2;  Length 416;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         96 IHRDVKPDN 104
              |||||||||
Db        125 IHRDVKPDN 133


RESULT 7
A46002
casein kinase I (EC 2.7.1.-) delta, 49K isoform - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46002
R;Graves, P.R.; Haas, D.W.; Hagedorn, C.H.; DePaoli-Roach, A.A.; Roach, P.J.
J. Biol. Chem. 268, 6394-6401, 1993
A;Title: Molecular cloning, expression, and characterization of a 49-kilodalton casein ki
A;Reference number: A46002; MUID:93203231; PMID:8454611
A;Accession: A46002
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-428 <GRA>
A;Cross-references: UNIPROT:Q06486; UNIPARC:UPI000012DC66; GB:L07578; NID:g294524; PIDN:
A;Experimental source: testis
A;Note: sequence extracted from NCBI backbone (NCBIN:127927, NCBIP:127928)
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: phosphotransferase; serine/threonine-specific protein kinase
F;7-279/Domain: protein kinase homology <KIN>

  Query Match             2.4%;  Score 9;  DB 2;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          96 IHRDVKPDN 104
               |||||||||
Db         125 IHRDVKPDN 133


RESULT 8
AI2045
serine/threonine kinase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AI2045
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-546 <KUR>
A;Cross-references: UNIPROT:Q8YVQ5; UNIPARC:UPI00000CE25F; GB:BA000019; PIDN:BAB73618.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1919

  Query Match             2.4%;  Score 9;  DB 2;  Length 546;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          97 HRDVKPDNI 105
               |||||||||
Db         137 HRDVKPDNI 145


RESULT 9
T25539
hypothetical protein C10H11.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25539
R;Dante, M.; Wamsley, P.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid C10H11.
A;Reference number: Z20047
A;Accession: T25539
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1173 <DAN>
A;Cross-references: UNIPROT:P92199; UNIPARC:UPI00000804C8; EMBL:U88311; PIDN:AAB42348.1;
A;Experimental source: strain Bristol N2; clone C10H11
C;Genetics:
A;Gene: CESP:C10H11.9
A;Map position: 1
A;Introns: 23/3; 51/1; 104/3; 343/1; 478/2; 868/3; 891/3; 970/3; 1027/3; 1114/1
C;Superfamily: hypothetical protein C10H11.9; protein kinase homology

  Query Match             2.4%;  Score 9;  DB 2;  Length 1173;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          96 IHRDVKPDN 104
               |||||||||
Db         187 IHRDVKPDN 195


RESULT 10
S74244
serine/threonine-specific protein kinase (EC 2.7.1.-) isoform I, Rho-associated - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 05-Oct-2004
C;Accession: S74244
R;Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A;Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein s
A;Reference number: S74244; MUID:96368048; PMID:8772201
A;Accession: S74244
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1354 <NAK>
A;Cross-references: UNIPROT:P70335; UNIPARC:UPI0000027020; EMBL:U58512; NID:g1514695; PII
C;Keywords: coiled coil; phosphotransferase; serine/threonine-specific protein kinase
F;74-338/Domain: protein kinase homology <KIN>
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

  Query Match             2.4%;  Score 9;  DB 2;  Length 1354;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          96 IHRDVKPDN 104
               |||||||||
Db         195 IHRDVKPDN 203


RESULT 11
S69211
serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - human
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 31-Dec-2004
C;Accession: S69211; S71910
R;Ishizaki, T.; Maekawa, M.; Fujisawa, K.; Okawa, K.; Iwamatsu, A.; Fujita, A.; Watanabe
EMBO J. 15, 1885-1893, 1996
A;Title: The small GTP-binding protein Rho binds to and activates a 160 kDa Ser/Thr prot
A;Reference number: S69211; MUID:96203110; PMID:8617235
A;Accession: S69211
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1354 <ISH1>
A;Cross-references: UNIPROT:Q13464; UNIPARC:UPI000006F0A4; EMBL:U43195; NID:g1276900; PI
A;Accession: S71910
A;Molecule type: protein
A;Residues: 187-195;281-288;465-473;573-587;818-828;885-893;934-945 <ISH2>
A;Cross-references: UNIPARC:UPI000017A400; UNIPARC:UPI000017A401; UNIPARC:UPI000017A402;
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;74-338/Domain: protein kinase homology <KIN>
F;82-90/Region: protein kinase ATP-binding motif
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

  Query Match             2.4%;  Score 9;  DB 2;  Length 1354;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          96 IHRDVKPDN 104
               |||||||||
Db         195 IHRDVKPDN 203


RESULT 12
S70633
serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - bovine
N;Alternate names: Rho-associated protein kinase
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
C;Accession: S70633; S77694
R;Matsui, T.; Amano, M.; Yamamoto, T.; Chihara, K.; Nakafuku, M.; Ito, M.; Nakano, T.; O
EMBO J. 15, 2208-2216, 1996
A;Title: Rho-associated kinase, a novel serine/threonine kinase, as a putative target fo
A;Reference number: S70633; MUID:96208507; PMID:8641286
A;Accession: S70633
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1388 <MAT1>
A;Cross-references: UNIPROT:Q28021; UNIPARC:UPI0000086C59; EMBL:U36909; NID:g1326077; PI
A;Accession: S77694
A;Molecule type: protein
A;Residues: 1-18;30-34;36-44;58-64;133-140;248-252;291-295;297-305;327-347;350-360;366-3
```

-1070 <MAT2>
A;Cross-references: UNIPARC:UPI000017A40B; UNIPARC:UPI000017A40C; UNIPARC:UPI000017A40D;
412; UNIPARC:UPI000017A413; UNIPARC:UPI000017A414; UNIPARC:UPI000017A415; UNIPARC:UPI000
I000017A41B; UNIPARC:UPI000017A41C; UNIPARC:UPI000017A41D; UNIPARC:UPI000017A41E; UNIPAR
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;90-354/Domain: protein kinase homology <KIN>
F;98-106/Region: protein kinase ATP-binding motif
F;1261-1315/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 2.4%; Score 9; DB 2; Length 1388;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 IHRDVKPDN 104
|||||||||
Db 211 IHRDVKPDN 219

RESULT 13
S74245
serine/threonine-specific protein kinase (EC 2.7.1.-) isoform II, Rho-associated - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 31-Dec-2004
C;Accession: S74245
R;Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A;Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein
A;Reference number: S74244; MUID:96368048; PMID:8772201
A;Accession: S74245
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1388 <NAK>
A;Cross-references: UNIPROT:P70336; UNIPARC:UPI0000027021; EMBL:U58513; NID:g1514697; PI
C;Keywords: phosphotransferase; serine/threonine-specific protein kinase
F;90-354/Domain: protein kinase homology <KIN>
F;1261-1315/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 2.4%; Score 9; DB 2; Length 1388;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 IHRDVKPDN 104
|||||||||
Db 211 IHRDVKPDN 219

RESULT 14
H88130
protein F10G7.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H88130
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: H88130
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <STO>
A;Cross-references: UNIPROT:Q19326; UNIPARC:UPI0000081869; GB:chr_II; PIDN:AA81128.1; PI
C;Genetics:
A;Gene: F10G7.3
A;Map position: 2

Query Match 2.2%; Score 8; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 344 AEPVEDEA 351
||||||||
Db 144 AEPVEDEA 151

RESULT 15
D84375
ATP phosphoribosyltransferase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84375
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lia
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: D84375
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-282 <STO>
A;Cross-references: UNIPROT:Q9HN53; UNIPARC:UPI000012C744; GB:AE004437; NID:g10581661; PI
C;Genetics:
A;Gene: hisG
C;Superfamily: ATP phosphoribosyltransferase; ATP phosphoribosyltransferase homology

Query Match 2.2%; Score 8; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 VPNKGRLH 261
||||||||
Db 5 VPNKGRLH 12

Search completed: May 9, 2006, 10:50:33
Job time : 24 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:49:27 ; Search time 230 Seconds
(without alignments)
1131.913 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 369
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	369	100.0	369	2	Q5T0Q5_HUMAN	Q5t0q5 homo sapien
2	369	100.0	486	2	Q86UX6_HUMAN	Q86ux6 homo sapien
3	300	81.3	381	2	Q5T0Q4_HUMAN	Q5t0q4 homo sapien
4	268	72.6	369	2	Q86UE1_HUMAN	Q86ue1 homo sapien
5	113	30.6	488	2	Q8QZV4_MOUSE	Q8qzv4 mus musculu
6	113	30.6	488	2	Q9JJG4_MOUSE	Q9jjg4 mus musculu
7	79	21.4	368	2	Q9BGT4_MACFA	Q9bgt4 macaca fasc
8	67	18.2	441	2	Q4RN62_TETNG	Q4rn62 tetraodon n
9	35	9.5	166	2	Q8WU08_HUMAN	Q8wu08 homo sapien
10	35	9.5	364	2	Q6UXH3_HUMAN	Q6uxh3 homo sapien
11	35	9.5	368	2	Q7TPQ4_MOUSE	Q7tpq4 mus musculu
12	35	9.5	396	2	Q5RAZ7_PONPY	Q5raz7 pongo pygma
13	35	9.5	396	2	Q6GQ72_XENLA	Q6gq72 xenopus lae
14	35	9.5	398	2	Q8BGW6_MOUSE	Q8bgw6 m mus muscu
15	35	9.5	414	2	Q8IY14_HUMAN	Q8iy14 homo sapien
16	35	9.5	414	2	Q9NY57_HUMAN	Q9ny57 homo sapien
17	35	9.5	414	2	Q7TMD3_MOUSE	Q7tmd3 mus musculu
18	35	9.5	414	2	Q8C4E0_MOUSE	Q8c4e0 mus musculu
19	35	9.5	414	2	Q9JJX8_MOUSE	Q9jjx8 mus musculu
20	30	8.1	367	2	Q4RZ50_TETNG	Q4rz50 tetraodon n
21	19	5.1	337	2	Q5RF90_PONPY	Q5rf90 pongo pygma
22	14	3.8	214	2	Q69YP0_HUMAN	Q69yp0 homo sapien
23	14	3.8	700	2	Q9VN23_DROME	Q9vn23 drosophila
24	13	3.5	338	2	O74426_SCHPO	O74426 schizosacch
25	12	3.3	311	2	Q6K1R8_ORYSA	Q6k1r8 oryza sativ
26	12	3.3	379	2	Q21483_CAEEL	Q21483 caenorhabdi
27	12	3.3	380	2	Q60Y37_CAEBR	Q60y37 caenorhabdi
28	11	3.0	210	2	Q5TV49_ANOGA	Q5tv49 anopheles g
29	11	3.0	278	2	Q7QFG8_ANOGA	Q7qfg8 anopheles g
30	11	3.0	509	2	Q4P7E0_USTMA	Q4p7e0 ustilago ma
31	11	3.0	824	2	Q6ZF83_ORYSA	Q6zf83 oryza sativ
32	10	2.7	270	2	Q6ULS3_SOYBN	Q6uls3 glycine max
33	10	2.7	282	2	Q949L9_BETVU	Q94919 beta vulgar
34	10	2.7	307	2	Q94EN6_SORBI	Q94en6 sorghum bic
35	10	2.7	311	2	Q5EC57_MAIZE	Q5ec57 zea mays (m
36	10	2.7	349	2	Q5EUH0_9PLAN	Q5euh0 gemmata sp.
37	10	2.7	567	2	Q52DZ2_MAGGR	Q52dz2 magnaporthe
38	10	2.7	567	2	Q4WMP1_ASPFU	Q4wmp1 aspergillus
39	10	2.7	629	2	Q5AVZ3_EMENI	Q5avz3 aspergillus
40	10	2.7	1158	2	Q7SCY3_NEUCR	Q7scy3 neurospora
41	10	2.7	1159	2	Q51TP5_MAGGR	Q51tp5 magnaporthe
42	10	2.7	1200	2	Q4IQS5_GIBZE	Q4iqs5 gibberella
43	9	2.4	97	2	Q5TV47_ANOGA	Q5tv47 anopheles g
44	9	2.4	127	2	Q5TV48_ANOGA	Q5tv48 anopheles g
45	9	2.4	144	2	P79278_PIG	P79278 sus scrofa

ALIGNMENTS

RESULT 1
Q5T0Q5_HUMAN
ID Q5T0Q5_HUMAN PRELIMINARY; PRT; 369 AA.
AC Q5T0Q5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Protein kinase (PKE).
GN Name=RP11-140A10.1; ORFNames=RP11-140A10.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL512622; CAI12187.1; -; Genomic_DNA.
DR Ensembl; ENSG00000165752; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 369 AA; 42425 MW; 83C54C4AF7D792E5 CRC64;

Query Match 100.0%; Score 369; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
                |||||||||
Db        361 PICPSAGSG 369


RESULT 2
Q86UX6_HUMAN
ID   Q86UX6_HUMAN PRELIMINARY;      PRT;   486 AA.
AC   Q86UX6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   PKE protein kinase.
GN   Name=STK32C; Synonyms=RP11-140A10.1; ORFNames=RP11-140A10.1-002;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ma A.-H., Nelson D.A., Xia L., Ravi L., Chen H.-C., Robinson D.R.,
RA   Kung H.-J.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Brown J.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AY098866; AAM21719.1; -; mRNA.
DR   EMBL; AL512622; CAI12181.1; -; Genomic_DNA.
DR   EMBL; AL590105; CAI13011.1; -; Genomic_DNA.
DR   EMBL; AL590105; CAI12181.1; JOINED; Genomic_DNA.
DR   EMBL; AL512622; CAI13011.1; JOINED; Genomic_DNA.
DR   HSSP; P31751; 1MRV.
DR   Ensembl; ENSG00000165752; Homo sapiens.
DR   HGNC; HGNC:21332; STK32C.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   486 AA;  54994 MW;  38FEFBB3863B21F3 CRC64;

  Query Match             100.0%;  Score 369;  DB 2;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 477

Qy        361 PICPSAGSG 369
                |||||||||
Db        478 PICPSAGSG 486


RESULT 3
Q5T0Q4_HUMAN
ID   Q5T0Q4_HUMAN PRELIMINARY;      PRT;   381 AA.
AC   Q5T0Q4;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Protein kinase (PKE).
GN   Name=RP11-140A10.1; ORFNames=RP11-140A10.1-004;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AL512622; CAI12188.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   381 AA;  43102 MW;  6564FFB4CDF5E333 CRC64;

  Query Match             81.3%;  Score 300;  DB 2;  Length 381;
  Best Local Similarity   100.0%;  Pred. No. 2e-285;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 116

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 176

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 236

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 296

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 356
```

RESULT 4
Q86UE1_HUMAN
ID Q86UE1_HUMAN PRELIMINARY; PRT; 369 AA.
AC Q86UE1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STK32C protein.
GN Name=STK32C;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RG NIH MGC Project;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC045760; AAH45760.1; -; mRNA.
DR HSSP; P31751; 1MRV.
DR Ensembl; ENSG00000165752; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 369 AA; 42395 MW; E152C66BB2D786B4 CRC64;

```
  Query Match             72.6%;  Score 268;  DB 2;  Length 369;
  Best Local Similarity   99.7%;  Pred. No. 5.2e-254;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLAVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||.
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369
```

RESULT 5
Q8QZV4_MOUSE
ID Q8QZV4_MOUSE PRELIMINARY; PRT; 488 AA.
AC Q8QZV4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Serine/threonine kinase 32C (Mus musculus adult male corpora
DE quadrigemina cDNA, RIKEN full-length enriched library,
DE clone:B230385A21 product:hypothetical serine/threonine protein kinase,
DE full insert sequence).
GN Name=Stk32c;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC026457; AAH26457.1; -; mRNA.
DR EMBL; AK046439; BAC32730.1; -; mRNA.
DR HSSP; P31751; 1MRV.
DR MGI; MGI:2385336; Stk32c.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 55263 MW; 2B6A927BE6B78EF2 CRC64;

Query Match 30.6%; Score 113; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.1e-101;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 170
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 229 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 288

Qy 171 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 223

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 341


RESULT 6
Q9JJG4_MOUSE
ID   Q9JJG4_MOUSE PRELIMINARY;      PRT;   488 AA.
AC   Q9JJG4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus brain cDNA, clone MNCb-1563, similar to AJ250840
DE   serine/threonine protein kinase (Mus musculus).
GN   Name=Stk32c; Synonyms=Pkek;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL;
RA   Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA   Hashimoto K.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AB041542; BAA95027.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   Ensembl; ENSMUSG00000015981; Mus musculus.
DR   MGI; MGI:2385336; Stk32c.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   488 AA;  55277 MW;  310483FF69E24E39 CRC64;

  Query Match             30.6%;  Score 113;  DB 2;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-101;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        111 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 288

Qy        171 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 341


RESULT 7
Q9BGT4_MACFA
ID   Q9BGT4_MACFA PRELIMINARY;      PRT;   368 AA.
AC   Q9BGT4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Frontal lobe left;
RA   Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB056389; BAB33045.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   368 AA;  42218 MW;  5D7269B32DABCC14 CRC64;

  Query Match             21.4%;  Score 79;  DB 2;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-68;
  Matches   79;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        253 FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLDAI 312
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLDAI 312

Qy        313 QQDFVIFNREKLKRSQDLP 331
              |||||||||||||||||||
Db        313 QQDFVIFNREKLKRSQDLP 331


RESULT 8
Q4RN62_TETNG
ID   Q4RN62_TETNG PRELIMINARY;      PRT;   441 AA.
AC   Q4RN62;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome undetermined SCAF15016, whole genome shotgun sequence.
GN   ORFNames=GSTENG00031718001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01015016; CAG10170.1; -; Genomic_DNA.
```

```
SQ   SEQUENCE   441 AA;  50816 MW;  71C81AC5A8E49E63 CRC64;

  Query Match             18.2%;  Score 67;  DB 2;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-56;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 125

Qy         61 LRYHLQQ 67
              |||||||
Db        126 LRYHLQQ 132


RESULT 9
Q8WU08_HUMAN
ID   Q8WU08_HUMAN PRELIMINARY;      PRT;   166 AA.
AC   Q8WU08;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Serine/threonine kinase 32A.
GN   Name=STK32A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Bladder;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Bladder;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC021666; AAH21666.1; -; mRNA.
DR   HSSP; P21146; 1OMW.
DR   Ensembl; ENSG00000169302; Homo sapiens.
DR   HGNC; HGNC:28317; STK32A.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   166 AA;  19792 MW;  CDCF94E54C793BA4 CRC64;

  Query Match             9.5%;  Score 35;  DB 2;  Length 166;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 10
Q6UXH3_HUMAN
ID   Q6UXH3_HUMAN PRELIMINARY;      PRT;   364 AA.
AC   Q6UXH3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   HSA250839.
GN   ORFNames=UNQ3003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358353; AAQ88719.1; -; mRNA.
DR   HSSP; P05132; 1APM.
DR   Ensembl; ENSG00000152953; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ   SEQUENCE   364 AA;  42195 MW;  FE52D0CB54C7A27C CRC64;

  Query Match             9.5%;  Score 35;  DB 2;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         32 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 66


RESULT 11
Q7TPQ4_MOUSE
```

```
ID   Q7TPQ4_MOUSE PRELIMINARY;      PRT;   368 AA.
AC   Q7TPQ4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Stk32a protein.
GN   Name=Stk32a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Olfactory epithelium;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Olfactory epithelium;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC055002; AAH55002.1; -; mRNA.
DR   HSSP; P31751; 1GZK.
DR   Ensembl; ENSMUSG00000039954; Mus musculus.
DR   MGI; MGI:2442403; Stk32a.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   368 AA;  43213 MW;  0DB7F6977C39BB56 CRC64;

  Query Match             9.5%;  Score 35;  DB 2;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 12
Q5RAZ7_PONPY
ID   Q5RAZ7_PONPY PRELIMINARY;      PRT;   396 AA.
AC   Q5RAZ7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein DKFZp469K2010.
GN   Name=DKFZp469K2010;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RG   The German cDNA Consortium;
RA   Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; CR858864; CAH91063.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   396 AA;  46340 MW;  2A8396C2E2A2E51B CRC64;

  Query Match             9.5%;  Score 35;  DB 2;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 13
Q6GQ72_XENLA
ID   Q6GQ72_XENLA PRELIMINARY;      PRT;   396 AA.
AC   Q6GQ72;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC80293 protein.
GN   Name=MGC80293;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
```

```
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC072876; AAH72876.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   396 AA;  45627 MW;  991810CE21523F85 CRC64;

  Query Match             9.5%;  Score 35;  DB 2;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 14
Q8BGW6_MOUSE
ID   Q8BGW6_MOUSE PRELIMINARY;      PRT;   398 AA.
AC   Q8BGW6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DE   enriched library, clone:9630050F05 product:SIMILAR TO SERINE THREONINE
DE   KINASE 32 homolog (Mus musculus 7 days neonate cerebellum cDNA, RIKEN
DE   full-length enriched library, clone:A730009C22 product:SIMILAR TO
DE   SERINE THREONINE KINASE 32 homolog) (Mus musculus adult retina cDNA,
DE   RIKEN full-length enriched library, clone:A930015B13 product:SIMILAR
DE   TO SERINE THREONINE KINASE 32 homolog).
GN   Name=Stk32a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
```

```
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AK036266; BAC29366.1; -; mRNA.
DR   EMBL; AK042599; BAC31302.1; -; mRNA.
DR   EMBL; AK044474; BAC31941.1; -; mRNA.
DR   HSSP; P31751; 1GZK.
DR   Ensembl; ENSMUSG00000039954; Mus musculus.
DR   MGI; MGI:2442403; Stk32a.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   398 AA;  46509 MW;  689BCA5B25CF18BB CRC64;

  Query Match             9.5%;  Score 35;  DB 2;  Length 398;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 15
Q8IY14_HUMAN
ID   Q8IY14_HUMAN PRELIMINARY;      PRT;   414 AA.
AC   Q8IY14;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Serine/threonine kinase 32B.
GN   Name=STK32B;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC038238; AAH38238.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   Ensembl; ENSG00000152953; Homo sapiens.
DR   HGNC; HGNC:14217; STK32B.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   414 AA;  47784 MW;  F0E5EE695FA8242F CRC64;

  Query Match             9.5%;  Score 35;  DB 2;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


Search completed: May  9, 2006, 10:54:39
Job time : 232 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:48:47 ; Search time 84 Seconds
(without alignments)
1930.128 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 369
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2442881

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	369	100.0	369	5	ABB84299	Abb84299 Human ser
2	369	100.0	369	7	ADJ70605	Adj70605 Human hea
3	369	100.0	486	8	ADJ96618	Adj96618 Human YAN
4	369	100.0	486	8	ADK71861	Adk71861 Human kin
5	337	91.3	485	5	AAE24141	Aae24141 Human kin
6	323	87.5	364	5	AAO17708	Aao17708 Human ser
7	300	81.3	375	4	AAE04371	Aae04371 Human kin
8	300	81.3	442	7	ADG74653	Adg74653 Human kin
9	269	72.9	713	5	ABB06090	Abb06090 Human NS
10	268	72.6	419	4	AAB65599	Aab65599 Novel pro
11	268	72.6	419	8	ADI29204	Adi29204 Human MAR
12	268	72.6	425	4	AAM40592	Aam40592 Human pol
13	254	68.8	429	4	AAB71961	Aab71961 Human TGF
14	217	58.8	419	4	AAM38806	Aam38806 Human pol
15	214	58.0	444	6	AAE37974	Aae37974 Human kin
16	209	56.6	488	6	ABO14992	Abo14992 Human NOV
17	113	30.6	384	6	ABU62279	Abu62279 Mouse ser
18	113	30.6	384	8	ADL09166	Adl09166 Mouse ser
19	113	30.6	384	9	ADZ58502	Adz58502 Mouse ser
20	113	30.6	399	5	ABB84300	Abb84300 Murine se
21	113	30.6	488	5	AAO17709	Aao17709 Murine se
22	79	21.4	368	5	ABB84301	Abb84301 Macaque s
23	35	9.5	160	4	AAU87204	Aau87204 Novel cen
24	35	9.5	160	8	ADI54519	Adi54519 Novel hum
25	35	9.5	225	5	AAE14258	Aae14258 Novel hum
26	35	9.5	236	5	AAE14259	Aae14259 Novel hum
27	35	9.5	253	9	AEA20331	Aea20331 Novel hum
28	35	9.5	327	4	AAU03504	Aau03504 Human pro
29	35	9.5	358	7	ADM03989	Adm03989 Human pro
30	35	9.5	364	4	AAU29309	Aau29309 Human PRO
31	35	9.5	364	6	ABU58685	Abu58685 Human PRO
32	35	9.5	364	6	ABU88233	Abu88233 Novel hum
33	35	9.5	364	6	ABU84548	Abu84548 Human sec
34	35	9.5	364	6	ABR66422	Abr66422 Human sec
35	35	9.5	364	6	ABR65812	Abr65812 Human sec
36	35	9.5	364	6	ABU99752	Abu99752 Human sec
37	35	9.5	364	6	ABU82991	Abu82991 Human PRO
38	35	9.5	364	6	ABU90112	Abu90112 Novel hum
39	35	9.5	364	6	ABR68361	Abr68361 Human sec
40	35	9.5	364	6	ABU96414	Abu96414 Novel hum
41	35	9.5	364	6	ABU92845	Abu92845 Human sec
42	35	9.5	364	6	ABO08922	Abo08922 Human sec
43	35	9.5	364	6	ABO02974	Abo02974 Human sec
44	35	9.5	364	6	ABR75128	Abr75128 Human sec
45	35	9.5	364	6	ABR94890	Abr94890 Human sec

ALIGNMENTS

RESULT 1
ABB84299
ID ABB84299 standard; protein; 369 AA.
XX
AC ABB84299;
XX
DT 12-NOV-2002 (first entry)
XX
DE Human serine/threonine protein kinase subfamily-related protein.
XX
KW Serine/threonine protein kinase subfamily; chromosome 10; human; enzyme;
KW cytostatic; gene therapy; drug screening; tissue typing; prostate; lung;
KW pharmacogenomic; brain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 42. .45
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 75. .77
FT /note= "protein kinase C phosphorylation site"
FT Region 95. .107
FT /note= "serine/threonine protein kinase active signature
FT motif"
FT Modified-site 152. .157
FT /note= "N-myristoylation site"
FT Region 185. .205
FT /note= "helix region"
FT Modified-site 226. .229
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 245. .247
FT /note= "protein kinase C phosphorylation site"
FT Modified-site 288. .291
FT /note= "N-glycosylation site"
FT Modified-site 298. .301
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 300. .303
FT /note= "casein kinase II phosphorylation site"
XX
PN WO200259288-A2.
XX
PD 01-AUG-2002.
XX
PF 15-JAN-2002; 2002WO-US000930.
XX
PR 23-JAN-2001; 2001US-0263162P.
PR 29-MAR-2001; 2001US-00819607.

XX
PA (PEKE) PE CORP NY.
XX
PI Beasley EM, Ye J, Yan C, Ketchum KA, Di Francesco V;
XX
DR WPI; 2002-599781/64.
DR N-PSDB; ABQ76181, ABQ76182.
XX
PT New peptides related to serine/threonine protein kinase subfamily, useful
PT for treating disorders associated with abnormal expression of kinase in
PT prostate, lungs and brain, in drug screening assays and pharmacogenomic
PT analysis.
XX
PS Claim 1; Fig 2A; 86pp; English.
XX
CC This invention describes a novel serine/threonine protein kinase
CC subfamily-associated protein isolated from human chromosome 10 which has
CC cytostatic activity and can be used for gene therapy. The products of the
CC invention are useful in substantial and specific assays related to
CC functional information of the peptide sequences, to raise antibodies or
CC to elicit immune response, as reagents in assays to determine the levels
CC of protein in biological fluids, and as markers for tissues where the
CC corresponding protein is expressed. The peptides and antibodies are
CC useful in drug screening assays, tissue typing and pharmacogenomic
CC analysis. They are also useful in treating disorders associated with the
CC absence of, inappropriate, or unwanted expression of kinase protein in
CC prostate, lungs or brain. The nucleic acid molecules are useful for
CC probes, primers and chemical intermediates in biological assays, for
CC constructing recombinant vectors, expressing antigenic portions of the
CC protein. The peptide and nucleic acid sequences are useful as models for
CC the development of human therapeutic targets, aid in the identification
CC of therapeutic proteins and serve as targets for the development of human
CC therapeutic agents that modulate kinase activity in cells and tissues
CC that express the kinase. The host cells are useful in producing a kinase
CC protein or peptide, and non-human transgenic animals. This sequence
CC represents the human serine/threonine protein kinase subfamily-associated
CC protein described in the disclosure of the invention
XX
SQ Sequence 369 AA;

Query Match 100.0%; Score 369; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369
```

RESULT 2
ADJ70605
ID ADJ70605 standard; protein; 369 AA.
XX
AC ADJ70605;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID2411.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 2411; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 369 AA;

Query Match 100.0%; Score 369; DB 7; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369
```

RESULT 3
ADJ96618
ID ADJ96618 standard; protein; 486 AA.
XX
AC ADJ96618;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human YANK3 protein SeqID 75.
XX
KW kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
KW PTK; STK; gene therapy; cancer; immune-related disease;
KW cardiovascular disease; brain; neuronal associated disease; metabolic;
KW inflammatory disorder; cytostatic; neuroprotective; immunomodulator;
KW antiinflammatory; enzyme; YANK3.
XX
OS Homo sapiens.
OS 28.
XX
PN WO2004006838-A2.
XX
PD 22-JAN-2004.
XX
PF 15-JUL-2003; 2003WO-US021730.
XX
PR 15-JUL-2002; 2002US-0395632P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Whyte D, Manning G, Caenepeel S;
XX
DR WPI; 2004-122753/12.
DR N-PSDB; ADJ96552.
XX
PT New nucleic acid molecule encoding a kinase polypeptide, useful for
PT preparing a composition for treating diseases or disorders, e.g., cancer,
PT or neurological, immunological or inflammatory disorders.
XX
PS Claim 1; SEQ ID NO 75; 366pp; English.
XX
CC This invention relates to a novel isolated, enriched or purified nucleic
CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
CC as well as protein kinase-like enzymes. The present invention describes
CC screening methods to identify agonists, antagonists and antibodies that
CC can be used to modulate the activity or function of the mammalian kinase
CC enzymes. As such, these compositions can be used for gene therapy
CC purposes to treat diseases or disorders including cancer, immune-related
CC diseases, cardiovascular disease, brain or neuronal associated disease,
CC metabolic and inflammatory disorders. Accordingly, they exhibit
CC cytostatic, neuroprotective, immunomodulator and antiinflammatory
CC activities. This polypeptide sequence is a human kinase protein sequence
CC of the invention.
XX
SQ Sequence 486 AA;

Query Match 100.0%; Score 369; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 477

Qy        361 PICPSAGSG 369
              |||||||||
Db        478 PICPSAGSG 486
```

RESULT 4
ADK71861
ID ADK71861 standard; protein; 486 AA.
XX
AC ADK71861;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human kinase and phosphatase KPP-38 protein.
XX
KW human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
KW hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV;
KW antiallergic; antiasthmatic; immunosuppressive; antithyroid;
KW dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal;
KW neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological;
KW antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;
KW antipsoriatic; haemostatic; cytostatic; antilipaemic; antiparasitic;
KW antihelmintic; antibacterial; virucide; protozoacide; fungicide;
KW cardiovascular disease; immune system; neurological; growth; development;
KW cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; enzyme;
KW single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO2004018641-A2.
XX
PD 04-MAR-2004.
XX
PF 25-AUG-2003; 2003WO-US026635.
XX
PR 26-AUG-2002; 2002US-0406172P.
PR 25-SEP-2002; 2002US-0413910P.
PR 27-SEP-2002; 2002US-0414296P.

```
PR   11-OCT-2002; 2002US-0417821P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Baughn MR,  Richardson TW,  Marquis JP,  Swarnakar A,  Tang YT;
PI   Becha SD,  Emerling BM,  Jin P,  Wilson AD,  Yue H,  Gietzen KJ;
PI   Chang H,  Yang YG,  Lee SY,  Khare R,  Elliott VS,  Hafalia AJA;
PI   Chawla NK,  Ramkumar J,  Gururajan R,  Tribouley CM,  Chien D,  Tran UK;
PI   Murage J;
XX
DR   WPI; 2004-226830/21.
DR   N-PSDB; ADK71920.
XX
PT   New human kinases and phosphatases, useful for diagnosing, treating or
PT   preventing atherosclerosis, hypertension, AIDS, allergy, multiple
PT   sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
PT   or hepatitis.
XX
PS   Claim 1; SEQ ID NO 38; 347pp; English.
XX
CC   The invention relates to a novel isolated polypeptide which is a human
CC   kinase and phosphatase (KPP). The polypeptide of the invention
CC   demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
CC   vasotropic, antiinflammatory, antianginal, anti-HIV, antiallergic,
CC   antiasthmatic, immunosuppressive, antithyroid, dermatological,
CC   antidiabetic, nephrotropic, antigout, gastrointestinal, neuroprotective,
CC   osteopathic, antiarthritic, uropathic, ophthalmological, antirheumatic,
CC   antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic,
CC   haemostatic, cytostatic, antilipaemic, antiparasitic, antihelmintic,
CC   antibacterial, virucide, protozoacide and fungicide activities. The
CC   kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and
CC   antagonists may be useful for diagnosing, treating or preventing
CC   disorders such as cardiovascular diseases, immune system disorders,
CC   neurological disorders, disorders affecting growth and development, cell
CC   proliferative disorders and viral, bacterial, fungal, parasitic,
CC   protozoan or helminthic infections. Furthermore, the molecules of the
CC   invention may be useful for creating transgenic animals to model human
CC   disease and during gene therapy. The current sequence is that of a human
CC   KPP protein of the invention.
XX
SQ   Sequence 486 AA;

  Query Match             100.0%;  Score 369;  DB 8;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 477

Qy        361 PICPSAGSG 369
              |||||||||
Db        478 PICPSAGSG 486
```

```
RESULT 5
AAE24141
ID   AAE24141 standard; protein; 485 AA.
XX
AC   AAE24141;
XX
DT   23-SEP-2002  (first entry)
XX
DE   Human kinase (PKIN)-12 protein.
XX
KW   Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;
KW   acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;
KW   asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;
KW   development; hepatitis; cardiovascular; hypertension; drug screening;
KW   myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;
KW   fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;
KW   hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hIV;
KW   neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;
KW   hyperlipidaemia; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .24
FT                   /label= Signal_peptide
FT   Protein         25. .485
FT                   /note= "Human mature kinase (PKIN)-12"
FT   Domain          65. .372
FT                   /note= "Protein kinase domain"
FT   Domain          93. .372
FT                   /note= "Protein kinase domain"
FT   Domain          93. .345
FT                   /note= "Eukaryotic protein kinase domain"
FT   Domain          95. .342
FT                   /note= "Protein kinase domain"
XX
PN   WO200233099-A2.
XX
PD   25-APR-2002.
XX
PF   20-OCT-2001; 2001WO-US047728.
XX
PR   20-OCT-2000; 2000US-0242410P.
PR   27-OCT-2000; 2000US-0244068P.
PR   03-NOV-2000; 2000US-0245708P.
PR   09-NOV-2000; 2000US-0247672P.
PR   16-NOV-2000; 2000US-0249565P.
PR   22-NOV-2000; 2000US-0252730P.
PR   01-DEC-2000; 2000US-0250807P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Gururajan R,  Baughn MR,  Walia NK,  Elliott VS,  Xu Y,  Arvizu C;
PI   Yao MG,  Ramkumar J,  Ding L,  Tang YT,  Hafalia AJA,  Nguyen DB;
PI   Gandhi AR,  Lu Y,  Yue H,  Burford N,  Bandman O,  Tribouley CM,  Lal PG;
PI   Recipon SA,  Lu DAM,  Borowsky ML,  Thornton M,  Swarnaker A;
PI   Thangavelu K,  Khan FA,  Ison CH;
XX
DR   WPI; 2002-454603/48.
DR   N-PSDB; AAD38855.
XX
PT   New human kinase polypeptide, for diagnosing, preventing and treating
PT   cancer, immune system disorders, growth and development disorders,
PT   cardiovascular disorders and lipid disorders.
XX
PS   Claim 1; Page 160-161; 210pp; English.
XX
CC   The invention relates human kinases (PKIN) and their corresponding
CC   nucleic acid sequences. PKIN and its DNA are useful for diagnosing,
CC   treating and preventing cancer, an immune system disorder (e.g., acquired
CC   immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,
```

```
CC   atherosclerosis, multiple sclerosis, psoriasis), disorders affecting
CC   growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),
CC   cardiovascular disorder (e.g., hypertension, myocardial infarction,
CC   Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,
CC   Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,
CC   hyperlipidaemia, obesity), and for assessing the effects of exogenous
CC   compounds. Anti-PKIN antibody is useful in a diagnostic test for a
CC   condition or a disease associated with the expression of PKIN in a
CC   biological sample. A composition comprising PKIN or an agonist or
CC   antagonist of PKIN is useful for treating a disease or condition
CC   associated with decreased or increased expression of functional PKIN.
CC   PKIN is useful in a number of drug screening techniques and to analyse
CC   the proteome of a tissue or cell type. PKIN DNA is useful for creating
CC   knockin humanised animals or transgenic animals to model human diseases,
CC   and in somatic or germline gene therapy. The present sequence is human
CC   PKIN protein
XX
SQ   Sequence 485 AA;

  Query Match             91.3%;  Score 337;  DB 5;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPA 337
              |||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPA 454


RESULT 6
AAO17708
ID   AAO17708 standard; protein; 364 AA.
XX
AC   AAO17708;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Human serine-threonine protein kinase.
XX
KW   Human; serine-threonine protein kinase; cancer; diabetes; obesity;
KW   central nervous system disorder; inflammation; gene therapy; COPD;
KW   neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;
KW   antidiabetic; antiallergic; antiasthmatic; antidepressant; anorectic;
KW   antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;
KW   enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200233056-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-EP011892.
XX
PR   16-OCT-2000; 2000US-0240097P.
PR   30-JUL-2001; 2001US-0308096P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Koehler RH;
XX
DR   WPI; 2002-435534/46.
DR   N-PSDB; AAL46714.
XX
PT   New human serine-threonine protein kinase and encoding polynucleotides,
PT   useful for diagnosing, treating and preventing central nervous system
PT   disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
XX
PS   Claim 25; Fig 2; 135pp; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   human serine-threonine protein kinase. The sequences can be used in the
CC   diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma
CC   or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or
CC   traumatic brain injury), diabetes, eating disorders (e.g. obesity,
CC   anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and
CC   chronic obstructive pulmonary disease (COPD). The present sequence is the
CC   protein of the invention
XX
SQ   Sequence 364 AA;

  Query Match             87.5%;  Score 323;  DB 5;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-309;
  Matches  323;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 72

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 132

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 192

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 252

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 312

Qy        301 ENDYLQDCLDAIQQDFVIFNREK 323
              |||||||||||||||||||||||
Db        313 ENDYLQDCLDAIQQDFVIFNREK 335


RESULT 7
AAE04371
ID   AAE04371 standard; protein; 375 AA.
XX
AC   AAE04371;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human kinase (PKIN)-12.
XX
KW   Human kinase; PKIN-12; therapy; immune disorder; Addison's disease; AIDS;
KW   acquired immune deficiency syndrome; growth and developmental disorder;
KW   arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma;
KW   leukaemia; cardiovascular disease; myocardial infarction; hypertension;
KW   lipid disorder; cancer; fatty liver; cholestasis; transgenic animal;
KW   gene therapy; antiallergic; antiasthmatic; antithyroid; dermatological;
KW   antidiabetic; nephrotophic; antiulcer; antiarthritic; antirheumatic;
```

```
KW   antipsoriatic; neuroprotective; cytostatic; hepatotrophic; osteopathic;
KW   vasotropic; antianginal; anorectic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          3. .305
FT                   /note= "Protein kinase domain"
FT   Domain          26. .278
FT                   /note= "Eukaryotic protein kinase domain"
FT   Domain          28. .275
FT                   /note= "Protein kinase domain"
FT   Binding-site    32. .55
FT                   /note= "Protein kinase ATP-binding domain"
FT   Domain          103. .116
FT                   /note= "Tyrosine kinase catalytic domain"
FT   Domain          139. .157
FT                   /note= "Tyrosine kinase catalytic domain"
FT   Region          145. .157
FT                   /note= "Protein kinase ST"
XX
PN   WO200146397-A2.
XX
PD   28-JUN-2001.
XX
PF   20-DEC-2000; 2000WO-US035304.
XX
PR   23-DEC-1999;   99US-0172066P.
PR   14-JAN-2000; 2000US-0176107P.
PR   21-JAN-2000; 2000US-0177731P.
PR   28-JAN-2000; 2000US-0178573P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yang J,  Baughn MR,  Burford N,  Au-Young J,  Lu DAM,  Reddy R;
PI   Yue H,  Yao MG,  Lal P,  Khan FA;
XX
DR   WPI; 2001-418059/44.
DR   N-PSDB; AAD08645.
XX
PT   Novel human kinase proteins (PKIN) useful for diagnosing, treating,
PT   preventing immune disorders, cardiovascular diseases and disorders
PT   affecting growth and development associated with abnormal expression of
PT   PKIN.
XX
PS   Claim 1; Page 118-119; 128pp; English.
XX
CC   The invention relates to novel human kinase proteins (PKIN) and nucleic
CC   acid molecules encoding them. PKIN is useful for identifying compounds
CC   that modulates its activity. PKIN cDNA is useful for assessing toxicity
CC   of a test compound. PKIN and its cDNA are useful for diagnosis,
CC   prevention and treatment of immune disorders such as acquired immune
CC   deficiency syndrome (AIDS), Addison's disease, anaemia, adult respiratory
CC   distress syndrome, allergies, amyloidosis, psoriasis, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, multiple sclerosis, asthma,
CC   osteoarthritis, osteoporosis, rheumatoid arthritis, ulcerative colitis
CC   and diabetes mellitus; growth and developmental disorders such as actinic
CC   keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis,
CC   hepatitis, mixed connective tissue disease (MCTD), and myelofibrosis;
CC   cancers such as adenocarcinoma and leukaemia, cardiovascular diseases
CC   such as myocardial infarction and hypertension; and lipid disorders such
CC   as fatty liver and cholestasis. PKIN cDNA is useful to detect upstream
CC   sequences such as promoters and regulatory elements, for creating knock
CC   in or knock out in humanised animals or transgenic animals to model human
CC   disease and for somatic or germline gene therapy for treating the above
CC   mentioned disorders. The present sequence is human kinase (PKIN)-12
XX
SQ   Sequence 375 AA;

  Query Match             81.3%;  Score 300;  DB 4;  Length 375;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-286;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350
```

```
RESULT 8
ADG74653
ID   ADG74653 standard; protein; 442 AA.
XX
AC   ADG74653;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human kinase and phosphatase protein (KPP) #10.
XX
KW   human; kinase and phosphatase; KPP; autoimmune disorder; obesity; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2003091419-A2.
XX
PD   06-NOV-2003.
XX
PF   24-APR-2003; 2003WO-US013124.
XX
PR   24-APR-2002; 2002US-0375539P.
PR   02-MAY-2002; 2002US-0378181P.
PR   24-MAY-2002; 2002US-0383182P.
XX
PA   (INCY-) INCYTE CORP.
PA   (LEES/) LEE S Y.
XX
PI   Mason PM,  Chang H,  Kamigaki LY,  Curtis AL,  Elliott VS,  Khare R;
PI   Richardson TW,  Kable AE,  Swarnakar A,  Marquis JP,  Ramkumar J;
PI   Hafalia AJA,  Tran UK,  Wilson AD,  Jin P,  Lindquist EA,  Jiang X;
PI   Jackson AA,  Gietzen KJ;
XX
DR   WPI; 2003-865587/80.
DR   N-PSDB; ADG74692.
XX
PT   New human kinases and phosphatases(KPP) polypeptide, useful for preparing
PT   a composition for treating a disease associated with decreased expression
PT   or overexpression of functional KPP e.g., cancer.
XX
PS   Claim 1; SEQ ID NO 10; 317pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of human
CC   kinase and phosphatase proteins (KPP's). The DNA and protein sequences of
CC   the invention are useful for treating a disease or condition associated
CC   with decreased expression or overexpression of functional KPP, such as:
CC   autoimmune disorders, obesity or cancer. The present amino acid sequence
CC   represents a human KPP of the invention.
XX
SQ   Sequence 442 AA;

  Query Match             81.3%;  Score 300;  DB 7;  Length 442;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-286;
```

```
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417


RESULT 9
ABB06090
ID   ABB06090 standard; protein; 713 AA.
XX
AC   ABB06090;
XX
DT   10-MAY-2002  (first entry)
XX
DE   Human NS protein sequence SEQ ID NO:182.
XX
KW   Human; cytostatic; osteopathic; gynaecological; neuroprotective;
KW   antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KW   vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW   anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
KW   antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
KW   anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic;
KW   gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
KW   contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KW   endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KW   rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW   inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW   infertility; cardiovascular disease; coagulation disease; hypertension;
KW   ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW   diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW   gastric ulcer; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200206315-A2.
XX
PD   24-JAN-2002.
XX
PF   17-JUL-2001; 2001WO-IL000653.
XX
PR   18-JUL-2000; 2000IL-00137345.
PR   15-DEC-2000; 2000IL-00140354.
XX
PA   (COMP-) COMPUGEN LTD.
XX
PI   Mintz L,  Freilich S,  Bernstein J;
XX
DR   WPI; 2002-155037/20.
DR   N-PSDB; ABL39744.
XX
PT   One hundred and twenty eight novel nucleic acid sequences, useful for
PT   treating and diagnosing e.g. cancer, asthma and Alzheimer's.
XX
PS   Claim 6; Page 207-209; 290pp; English.
XX
CC   ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC   encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC   (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC   antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC   vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC   anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
CC   anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant,
CC   immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer,
CC   antidepressant, gastrointestinal, aeuroleptic, cerebroprotective,
CC   nootropic and contraceptive activities. The NS can be used in vaccines,
CC   gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC   antibodies from the present invention can be used for treating and
CC   diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC   diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC   cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC   glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC   disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC   disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC   depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC   Alzheimer's disease and as a contraceptive
XX
SQ   Sequence 713 AA;

  Query Match             72.9%;  Score 269;  DB 5;  Length 713;
  Best Local Similarity   100.0%;  Pred. No. 8e-256;
  Matches  269;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         32 EHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTVRLYICEMALALDYLR 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 EHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTVRLYICEMALALDYLR 250

Qy         92 GQHIIHRDVKPDNILLDERGHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNG 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 GQHIIHRDVKPDNILLDERGHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNG 310

Qy        152 GTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVAL 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVAL 370

Qy        212 LRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPGFVPNKGRLHCDPTFELEEM 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 LRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPGFVPNKGRLHCDPTFELEEM 430

Qy        272 ILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              |||||||||||||||||||||||||||||
Db        431 ILESRPLHKKKKRLAKNKSRDNSRDSSQS 459


RESULT 10
AAB65599
ID   AAB65599 standard; protein; 419 AA.
XX
AC   AAB65599;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Novel protein kinase, SEQ ID NO: 124.
XX
KW   Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW   immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW   dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW   immune disorder; cardiovascular disease; neurodegenerative disease;
KW   cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW   inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS   Homo sapiens.
XX
PN   WO200073469-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US014842.
XX
PR   28-MAY-1999;   99US-0136503P.
```

```
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Martinez R,  Whyte D,  Sudersanam S;
XX
DR   WPI; 2001-032161/04.
DR   N-PSDB; AAF44624.
XX
PT   Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT   treating immune-related diseases and disorders, cardiovascular disease,
PT   neurodegenerative diseases and/or cancers.
XX
PS   Claim 10; Fig 1; 310pp; English.
XX
CC   The present sequence is a novel protein kinase. The novel protein kinases
CC   and the nucleic acids that encode them may be used in the treatment and
CC   diagnosis of diseases associated with inappropriate kinase expression
CC   such as immune-related diseases and disorders, cardiovascular disease,
CC   neurodegenerative diseases and/or cancers. The nucleic acids and
CC   complementary sequences may also be used as DNA probes in diagnostic
CC   assays. The kinase polypeptides may be used as antigens in the production
CC   of antibodies of kinase expression and activity. Anti-kinase antibodies
CC   and kinase antagonists may also be used to down regulate kinase
CC   expression and activity. Diseases related to kinase expression and
CC   activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC   disorders, complications of organ transplantation, myocardial infarction,
CC   immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC   stress related disorders, chronic inflammatory bowel disease, chronic
CC   inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC   psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC   disorders
XX
SQ   Sequence 419 AA;

  Query Match             72.6%;  Score 268;  DB 4;  Length 419;
  Best Local Similarity   99.7%;  Pred. No. 4.7e-255;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFXSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 11
ADI29204
ID   ADI29204 standard; protein; 419 AA.
XX
AC   ADI29204;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human MARK3-associated protein #2.
XX
KW   Human; antisense gene therapy; MARK3;
KW   MAP/microtubule affinity-regulating kinase 3; cancer;
KW   Alzheimer's disease; neurodegenerative disorde;
KW   hyperproliferative disorder; cytostatic.
XX
OS   Homo sapiens.
XX
PN   US2003232771-A1.
XX
PD   18-DEC-2003.
XX
PF   17-JUN-2002; 2002US-00174319.
XX
PR   17-JUN-2002; 2002US-00174319.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ward DT,  Freier SM,  Dobie KW;
XX
DR   WPI; 2004-052188/05.
DR   N-PSDB; ADI29322.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   microtubule-affinity-regulating kinases (MARK3), useful for modulating
PT   expression of MARK3 or for treating cancer or Alzheimer's disease.
XX
PS   Disclosure; SEQ ID NO 124; 233pp; English.
XX
CC   The invention relates to a compound comprising a sequence comprising 8-80
CC   base pairs (bp) targeted to a nucleic acid encoding MARK3
CC   (MAP/microtubule affinity-regulating kinase 3), that specifically
CC   hybridises with the nucleic acid encoding MARK3 and inhibits expression
CC   of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
CC   composition comprising the compound and a carrier or diluent, inhibiting
CC   the expression of MARK3 in cells or tissues, treating an animal having or
CC   suspected of having a disease or condition associated with MARK3 and
CC   screening for an antisense compound. The antisense oligonucleotide is
CC   useful for preparing a composition for treating hyperproliferative
CC   disorder, particularly cancer and neurodegenerative diseases e.g.
CC   Alzheimer's disease. The present sequence is a MARK3 associated protein
CC   included in the figures but not mentioned anywhere else in the
CC   specification.
XX
SQ   Sequence 419 AA;

  Query Match             72.6%;  Score 268;  DB 8;  Length 419;
  Best Local Similarity   99.7%;  Pred. No. 4.7e-255;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFXSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350
```

```
Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 12
AAM40592
ID   AAM40592 standard; protein; 425 AA.
XX
AC   AAM40592;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 5523.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI59748.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Example 2; SEQ ID NO 5523; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 425 AA;

  Query Match             72.6%;  Score 268;  DB 4;  Length 425;
  Best Local Similarity   99.7%;  Pred. No. 4.8e-255;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 116

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 176

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        177 ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 236

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 296

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 356

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 416

Qy        361 PICPSAGSG 369
              |||||||||
Db        417 PICPSAGSG 425


RESULT 13
AAB71961
ID   AAB71961 standard; protein; 429 AA.
XX
AC   AAB71961;
XX
DT   11-MAY-2001  (first entry)
XX
DE   Human TGF-beta receptor encoded by cDNA clone HTEMH65.
XX
KW   Human; antisclerotic; dermatological; immunosuppressive; cytostatic;
KW   antiinflammatory; anti-HIV; immunostimulant; cardiant; vascular;
KW   ophthalmological; neuroprotective; nootropic; anticonvulsant; vaccine;
KW   antiparkinsonian; antimicrobial; vulnerary; gene therapy; infection;
KW   transforming growth factor; TGF; TGF-beta receptor; immune disorder;
KW   hyperproliferative disorder; cardiovascular disease; angiogenesis;
KW   neurological disorder.
XX
OS   Homo sapiens.
XX
PN   WO200112670-A1.
XX
PD   22-FEB-2001.
XX
PF   10-AUG-2000; 2000WO-US021736.
XX
PR   13-AUG-1999;   99US-0148682P.
PR   20-SEP-1999;   99US-0154887P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J;
XX
DR   WPI; 2001-202858/20.
DR   N-PSDB; AAF75340.
XX
PT   Nucleic acid molecules encoding 12 transforming growth factor-beta
```

```
PT   receptor polypeptides, useful for preventing, diagnosing and treating
PT   e.g. cancers, Parkinson's disease and diabetic retinopathy.
XX
PS   Claim 11; Page 299-300; 311pp; English.
XX
CC   The present sequence is one of 12 novel human transforming growth factor
CC   (TGF)-beta receptor polypeptides. The TGF-beta receptor polynucleotides
CC   and polypeptides may be used in the prevention, diagnosis and treatment
CC   of diseases associated with inappropriate polypeptide expression. Such
CC   diseases include immune disorders (e.g. multiple sclerosis, systemic
CC   lupus erythematosus and human immuno-deficiency virus (HIV) infections),
CC   hyperproliferative disorders (e.g. cancers and Gaucher's disease),
CC   cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy
CC   and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft
CC   neovascularisation and diabetic retinopathy), neurological disorders
CC   (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease)
CC   and infectious diseases. The polynucleotides and polypeptides are also
CC   useful for promoting wound healing, regeneration and/or chemotaxis. The
CC   polynucleotides and their complementary sequences may also be used as DNA
CC   probes in diagnostic assays to detect and quantitate the presence of
CC   similar nucleic acid sequences in samples. The polypeptides may be used
CC   as antigens in the production of antibodies and in assays to identify
CC   modulators of protein expression and activity. The anti-TGF-beta receptor
CC   antibodies may be used to down regulate expression and activity and as
CC   diagnostic agents for detecting the presence of the polypeptides in
CC   samples
XX
SQ   Sequence 429 AA;

  Query Match             68.8%;  Score 254;  DB 4;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-241;
  Matches  254;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          83 MALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATIIKDGERATALAGTKPYMAP 142
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATIIKDGERATALAGTKPYMAP 60

Qy         143 EIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVP 202
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVP 120

Qy         203 TWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPGFVPNKGRLHC 262
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPGFVPNKGRLHC 180

Qy         263 DPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLDAIQQDFVIFNRE 322
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 DPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLDAIQQDFVIFNRE 240

Qy         323 KLKRSQDLPREPLP 336
               ||||||||||||||
Db         241 KLKRSQDLPREPLP 254


RESULT 14
AAM38806
ID   AAM38806 standard; protein; 419 AA.
XX
AC   AAM38806;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 1951.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI57962.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Example 3; SEQ ID NO 1951; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 419 AA;

  Query Match             58.8%;  Score 217;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 9e-205;
  Matches  217;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         153 TGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALL 212
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         203 TGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALL 262

Qy         213 RKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMI 272
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         263 RKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMI 322

Qy         273 LESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPR 332
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         323 LESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPR 382

Qy         333 EPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG 369
               |||||||||||||||||||||||||||||||||||||
Db         383 EPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG 419


RESULT 15
AAE37974
ID   AAE37974 standard; protein; 444 AA.
XX
```

```
AC   AAE37974;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human kinase and phosphatase (KPP-19) protein.
XX
KW   Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;
KW   atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;
KW   psoriasis; thromobocytopaenia; developmental disorder; Reiter's syndrome;
KW   renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;
KW   neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;
KW   autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;
KW   acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;
KW   nootropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;
KW   allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;
KW   osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;
KW   gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
XX
OS   Homo sapiens.
XX
PN   WO2003050084-A2.
XX
PD   19-JUN-2003.
XX
PF   06-DEC-2002; 2002WO-US039126.
XX
PR   07-DEC-2001; 2001US-0340235P.
PR   19-DEC-2001; 2001US-0343007P.
PR   21-DEC-2001; 2001US-0343546P.
PR   04-FEB-2002; 2002US-0354388P.
PR   15-FEB-2002; 2002US-0357675P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Kable AE,  Chien D,  Wilson AD,  Swarnakar A,  Gorvad AE;
PI   Hafalia AJA,  Emerling BM,  Ramkumar J,  Jin P,  Griffin JA,  Marquis JP;
PI   Baughn MR,  Chawla NK,  Lehr-Mason PM,  Khare R,  Lee S,  Hawkins PR;
PI   Becha SD,  Lee SY,  Sprague WW,  Zebarjadian Y;
XX
DR   WPI; 2003-532894/50.
DR   N-PSDB; AAD57346.
XX
PT   New human kinases and phosphatases and polynucleotides, useful for
PT   diagnosing, treating or preventing autoimmune or inflammatory disorders
PT   (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT   cancer or hepatitis.
XX
PS   Claim 1; Page 224-225; 282pp; English.
XX
CC   The invention relates to an isolated polypeptide, which is a human kinase
CC   and phosphatase (KPP). KPP agonists and antagonists are useful for
CC   diagnosing, treating or preventing disorders associated with aberrant
CC   expression of KPP, particularly cell proliferative disorders (e.g.
CC   arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
CC   nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
CC   thromobocytopaenia or cancer), developmental disorders (eg. renal tubular
CC   acidosis, anaemia or mental retardation), neurological disorders (e.g.
CC   Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/
CC   inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,
CC   allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
CC   disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
CC   gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,
CC   multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC   syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC   bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP
CC   is useful in assessing the effects of exogenous compounds on the
CC   expression of nucleic acids and kinases and phosphatases. KPP gene is
CC   useful in gene therapy and for creating transgenic animals to model human
CC   disease. The present sequence is human KPP protein
XX
SQ   Sequence 444 AA;

  Query Match             58.0%;  Score 214;  DB 6;  Length 444;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-202;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRK 214
              ||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRK 331


Search completed: May  9, 2006, 10:50:43
Job time : 86 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:50:09 ; Search time 19 Seconds
(without alignments)
1605.649 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 369
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 1

Total number of hits satisfying chosen parameters: 570988

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	369	100.0	369	2	US-09-819-607-2	Sequence 2, Appli
2	369	100.0	419	2	US-09-799-875-14	Sequence 14, Appl
3	113	30.6	384	2	US-09-801-876B-6	Sequence 6, Appli
4	113	30.6	384	2	US-10-254-869-6	Sequence 6, Appli
5	113	30.6	384	2	US-10-667-442-6	Sequence 6, Appli
6	113	30.6	399	2	US-09-819-607-4	Sequence 4, Appli
7	79	21.4	368	2	US-09-819-607-5	Sequence 5, Appli
8	35	9.5	225	2	US-09-841-683-5	Sequence 5, Appli
9	35	9.5	225	2	US-10-620-845-5	Sequence 5, Appli
10	35	9.5	236	2	US-09-841-683-7	Sequence 7, Appli
11	35	9.5	236	2	US-10-620-845-7	Sequence 7, Appli
12	35	9.5	396	2	US-09-801-876B-2	Sequence 2, Appli
13	35	9.5	396	2	US-09-841-683-11	Sequence 11, Appl
14	35	9.5	396	2	US-10-254-869-2	Sequence 2, Appli
15	35	9.5	396	2	US-10-667-442-2	Sequence 2, Appli
16	35	9.5	396	2	US-10-620-845-11	Sequence 11, Appl
17	35	9.5	403	2	US-09-801-876B-5	Sequence 5, Appli
18	35	9.5	403	2	US-10-254-869-5	Sequence 5, Appli
19	35	9.5	403	2	US-10-667-442-5	Sequence 5, Appli
20	35	9.5	404	2	US-09-801-876B-4	Sequence 4, Appli
21	35	9.5	404	2	US-10-254-869-4	Sequence 4, Appli
22	35	9.5	404	2	US-10-667-442-4	Sequence 4, Appli
23	35	9.5	407	2	US-09-841-683-9	Sequence 9, Appli
24	35	9.5	407	2	US-10-620-845-9	Sequence 9, Appli
25	29	7.9	316	2	US-09-801-876B-7	Sequence 7, Appli
26	29	7.9	316	2	US-10-254-869-7	Sequence 7, Appli
27	29	7.9	316	2	US-10-667-442-7	Sequence 7, Appli
28	14	3.8	178	2	US-09-270-767-31704	Sequence 31704, A
29	14	3.8	178	2	US-09-270-767-46921	Sequence 46921, A
30	12	3.3	347	2	US-09-801-876B-8	Sequence 8, Appli
31	12	3.3	347	2	US-10-254-869-8	Sequence 8, Appli
32	12	3.3	347	2	US-10-667-442-8	Sequence 8, Appli
33	9	2.4	128	2	US-09-270-767-33111	Sequence 33111, A
34	9	2.4	128	2	US-09-270-767-48328	Sequence 48328, A
35	9	2.4	378	2	US-09-771-161A-130	Sequence 130, App
36	9	2.4	399	2	US-09-813-818-4	Sequence 4, Appli
37	9	2.4	399	2	US-10-199-333-4	Sequence 4, Appli
38	9	2.4	401	2	US-09-813-818-3	Sequence 3, Appli
39	9	2.4	401	2	US-10-199-333-3	Sequence 3, Appli
40	9	2.4	409	2	US-09-813-818-2	Sequence 2, Appli
41	9	2.4	409	2	US-10-199-333-2	Sequence 2, Appli
42	9	2.4	415	1	US-08-454-097-35	Sequence 35, Appl
43	9	2.4	415	2	US-08-185-359-35	Sequence 35, Appl
44	9	2.4	415	2	US-09-457-040B-22	Sequence 22, Appl
45	9	2.4	415	2	US-09-538-092-1145	Sequence 1145, Ap

ALIGNMENTS

RESULT 1
US-09-819-607-2
; Sequence 2, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
US-09-819-607-2

Query Match 100.0%; Score 369; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
```

```
Db        361 PICPSAGSG 369


RESULT 2
US-09-799-875-14
; Sequence 14, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
;  APPLICANT:  Meyers, Rachel
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Williamson, Mark
;  TITLE OF INVENTION:  No. 6638721el Human Protein Kinases and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE:  35800/209996
;  CURRENT APPLICATION NUMBER: US/09/799,875
;  CURRENT FILING DATE:  2001-03-06
;  PRIOR APPLICATION NUMBER:  60/182,059
;  PRIOR FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  09/659,287
;  PRIOR FILING DATE:  2000-09-12
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-799-875-14

  Query Match             100.0%;  Score 369;  DB 2;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 3
US-09-801-876B-6
; Sequence 6, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160
;  CURRENT APPLICATION NUMBER: US/09/801,876B
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-09-801-876B-6

  Query Match             30.6%;  Score 113;  DB 2;  Length 384;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-100;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        111 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 212

Qy        171 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 265


RESULT 4
US-10-254-869-6
; Sequence 6, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV
;  CURRENT APPLICATION NUMBER: US/10/254,869
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-254-869-6

  Query Match             30.6%;  Score 113;  DB 2;  Length 384;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-100;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        111 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 212

Qy        171 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 265


RESULT 5
US-10-667-442-6
; Sequence 6, Application US/10667442
; Patent No. 6821765
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV II
;  CURRENT APPLICATION NUMBER: US/10/667,442
;  CURRENT FILING DATE:  2003-09-23
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-667-442-6
```

```
  Query Match             30.6%;  Score 113;  DB 2;  Length 384;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-100;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        111 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 212

Qy        171 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 265


RESULT 6
US-09-819-607-4
; Sequence 4, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001078
;  CURRENT APPLICATION NUMBER: US/09/819,607
;  CURRENT FILING DATE:  2001-03-29
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 399
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-819-607-4

  Query Match             30.6%;  Score 113;  DB 2;  Length 399;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-100;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        111 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 200

Qy        171 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 253


RESULT 7
US-09-819-607-5
; Sequence 5, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001078
;  CURRENT APPLICATION NUMBER: US/09/819,607
;  CURRENT FILING DATE:  2001-03-29
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-09-819-607-5

  Query Match             21.4%;  Score 79;  DB 2;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-67;
  Matches   79;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        253 FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLDAI 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLDAI 312

Qy        313 QQDFVIFNREKLKRSQDLP 331
              |||||||||||||||||||
Db        313 QQDFVIFNREKLKRSQDLP 331


RESULT 8
US-09-841-683-5
; Sequence 5, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/09/841,683
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-841-683-5

  Query Match              9.5%;  Score 35;  DB 2;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 9
US-10-620-845-5
; Sequence 5, Application US/10620845
; Patent No. 6908758
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: No. 6908758el Human Kinase Proteins and Polynucleotides Encoding
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/10/620,845
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-620-845-5

  Query Match              9.5%;  Score 35;  DB 2;  Length 225;
```

```
  Best Local Similarity   100.0%;  Pred. No. 2.5e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 10
US-09-841-683-7
; Sequence 7, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/09/841,683
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-841-683-7

  Query Match             9.5%;  Score 35;  DB 2;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 11
US-10-620-845-7
; Sequence 7, Application US/10620845
; Patent No. 6908758
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: No. 6908758el Human Kinase Proteins and Polynucleotides Encoding
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/10/620,845
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-620-845-7

  Query Match             9.5%;  Score 35;  DB 2;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 12
US-09-801-876B-2
; Sequence 2, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160
;  CURRENT APPLICATION NUMBER: US/09/801,876B
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: Human
US-09-801-876B-2

  Query Match             9.5%;  Score 35;  DB 2;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 13
US-09-841-683-11
; Sequence 11, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding t
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/09/841,683
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-841-683-11

  Query Match             9.5%;  Score 35;  DB 2;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116
```

```
RESULT 14
US-10-254-869-2
; Sequence 2, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV
;  CURRENT APPLICATION NUMBER: US/10/254,869
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: Human
US-10-254-869-2

  Query Match             9.5%;  Score 35;  DB 2;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 15
US-10-667-442-2
; Sequence 2, Application US/10667442
; Patent No. 6821765
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV II
;  CURRENT APPLICATION NUMBER: US/10/667,442
;  CURRENT FILING DATE:  2003-09-23
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-667-442-2

  Query Match             9.5%;  Score 35;  DB 2;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-25;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


Search completed: May  9, 2006, 10:50:56
Job time : 19 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:50:45 ; Search time 49 Seconds
(without alignments)
3146.511 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 369
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 1

Total number of hits satisfying chosen parameters: 1866650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	369	100.0	369	3	US-09-819-607-2	Sequence 2, Appli
2	369	100.0	369	4	US-10-074-978A-155	Sequence 155, App
3	369	100.0	369	4	US-10-633-631-2	Sequence 2, Appli
4	369	100.0	369	4	US-10-408-765A-2411	Sequence 2411, Ap
5	369	100.0	419	3	US-09-799-875-14	Sequence 14, Appl
6	369	100.0	419	4	US-10-303-664A-6	Sequence 6, Appli
7	369	100.0	419	4	US-10-649-156-14	Sequence 14, Appl
8	369	100.0	486	4	US-10-618-941-75	Sequence 75, Appl
9	337	91.3	485	4	US-10-415-011-12	Sequence 12, Appl
10	300	81.3	375	4	US-10-168-582-12	Sequence 12, Appl
11	209	56.6	255	4	US-10-074-978A-161	Sequence 161, App
12	209	56.6	258	4	US-10-074-978A-159	Sequence 159, App
13	209	56.6	488	4	US-10-074-978A-18	Sequence 18, Appl
14	191	51.8	215	4	US-10-074-978A-163	Sequence 163, App
15	113	30.6	384	3	US-09-801-876B-6	Sequence 6, Appli
16	113	30.6	384	4	US-10-254-869-6	Sequence 6, Appli
17	113	30.6	384	4	US-10-667-442-6	Sequence 6, Appli
18	113	30.6	384	5	US-10-962-625-6	Sequence 6, Appli
19	113	30.6	399	3	US-09-819-607-4	Sequence 4, Appli
20	113	30.6	399	4	US-10-633-631-4	Sequence 4, Appli
21	113	30.6	488	4	US-10-074-978A-154	Sequence 154, App
22	79	21.4	368	3	US-09-819-607-5	Sequence 5, Appli
23	79	21.4	368	4	US-10-074-978A-156	Sequence 156, App
24	79	21.4	368	4	US-10-633-631-5	Sequence 5, Appli
25	35	9.5	160	3	US-09-764-875-722	Sequence 722, App
26	35	9.5	225	3	US-09-841-683-5	Sequence 5, Appli
27	35	9.5	225	4	US-10-620-845-5	Sequence 5, Appli
28	35	9.5	236	3	US-09-841-683-7	Sequence 7, Appli
29	35	9.5	236	4	US-10-620-845-7	Sequence 7, Appli
30	35	9.5	358	4	US-10-108-260A-2674	Sequence 2674, Ap
31	35	9.5	364	4	US-10-052-586-572	Sequence 572, App
32	35	9.5	364	4	US-10-174-590-572	Sequence 572, App
33	35	9.5	364	4	US-10-176-758-572	Sequence 572, App
34	35	9.5	364	4	US-10-175-737-572	Sequence 572, App
35	35	9.5	364	4	US-10-174-581-572	Sequence 572, App
36	35	9.5	364	4	US-10-176-483-572	Sequence 572, App
37	35	9.5	364	4	US-10-176-749-572	Sequence 572, App
38	35	9.5	364	4	US-10-176-914-572	Sequence 572, App
39	35	9.5	364	4	US-10-176-915-572	Sequence 572, App
40	35	9.5	364	4	US-10-173-706-572	Sequence 572, App
41	35	9.5	364	4	US-10-175-738-572	Sequence 572, App
42	35	9.5	364	4	US-10-175-752-572	Sequence 572, App
43	35	9.5	364	4	US-10-176-482-572	Sequence 572, App
44	35	9.5	364	4	US-10-176-757-572	Sequence 572, App
45	35	9.5	364	4	US-10-176-913-572	Sequence 572, App

ALIGNMENTS

RESULT 1
US-09-819-607-2
; Sequence 2, Application US/09819607
; Publication No. US20030022337A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
US-09-819-607-2

Query Match 100.0%; Score 369; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
```

```
Db        361 PICPSAGSG 369


RESULT 2
US-10-074-978A-155
; Sequence 155, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-074-978A-155

  Query Match           100.0%;  Score 369;  DB 4;  Length 369;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369


RESULT 3
US-10-633-631-2
; Sequence 2, Application US/10633631
; Publication No. US20040067568A1
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001078DIV
;  CURRENT APPLICATION NUMBER: US/10/633,631
;  CURRENT FILING DATE:  2003-08-05
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-633-631-2

  Query Match           100.0%;  Score 369;  DB 4;  Length 369;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
```

```
Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369


RESULT 4
US-10-408-765A-2411
; Sequence 2411, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2411
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-2411

  Query Match             100.0%;  Score 369;  DB 4;  Length 369;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369


RESULT 5
US-09-799-875-14
; Sequence 14, Application US/09799875
; Patent No. US20020034780A1
; GENERAL INFORMATION:
;  APPLICANT:  Meyers, Rachel
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Williamson, Mark
;  TITLE OF INVENTION:  No. US20020034780A1el Human Protein Kinases and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE:  35800/209996
;  CURRENT APPLICATION NUMBER: US/09/799,875
;  CURRENT FILING DATE:  2001-03-06
;  PRIOR APPLICATION NUMBER:  60/182,059
;  PRIOR FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  09/659,287
;  PRIOR FILING DATE:  2000-09-12
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-799-875-14

  Query Match             100.0%;  Score 369;  DB 3;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 6
US-10-303-664A-6
; Sequence 6, Application US/10303664A
; Publication No. US20030153018A1
; GENERAL INFORMATION:
;  APPLICANT: Hunter, John Joseph
;  APPLICANT:  Williamson, Mark W.
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Rudolph-Owen, Laura A.
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;  TITLE OF INVENTION:  CANCER USING  2192, 2193, 6568, 8895, 9138, 9217, 9609,
;  TITLE OF INVENTION:  9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,
;  TITLE OF INVENTION:  33794, 54476 and 94710
;  FILE REFERENCE: MPI2001-290P3R(M)
;  CURRENT APPLICATION NUMBER: US/10/303,664A
;  CURRENT FILING DATE:  2002-11-25
```

```
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-303-664A-6

  Query Match             100.0%;  Score 369;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 7
US-10-649-156-14
; Sequence 14, Application US/10649156
; Publication No. US20040038346A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Williamson, Mark
;  TITLE OF INVENTION: No. US20040038346A1el Human Protein Kinases and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 35800/209996
;  CURRENT APPLICATION NUMBER: US/10/649,156
;  CURRENT FILING DATE:  2003-08-27
;  PRIOR APPLICATION NUMBER: US/09/799,875
;  PRIOR FILING DATE: 2001-03-06
;  PRIOR APPLICATION NUMBER: 60/182,059
;  PRIOR FILING DATE: 2000-02-11
;  PRIOR APPLICATION NUMBER: 09/659,287
;  PRIOR FILING DATE: 2000-09-12
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-649-156-14

  Query Match             100.0%;  Score 369;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 8
US-10-618-941-75
; Sequence 75, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
;  APPLICANT: WHYTE, DAVID
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  CAENEPEEL, SEAN
;  TITLE OF INVENTION: NOVEL KINASES
;  FILE REFERENCE: 034536-0321
;  CURRENT APPLICATION NUMBER: US/10/618,941
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: 60/395,632
;  PRIOR FILING DATE: 2002-07-15
;  NUMBER OF SEQ ID NOS: 143
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
;   LENGTH: 486
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-618-941-75

  Query Match             100.0%;  Score 369;  DB 4;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417
```

```
Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 477

Qy        361 PICPSAGSG 369
              |||||||||
Db        478 PICPSAGSG 486


RESULT 9
US-10-415-011-12
; Sequence 12, Application US/10415011
; Publication No. US20040053394A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE CORPORATION
;  APPLICANT:  GURURAJAN, Rajagopal
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  ELLIOTT, Vicki S.
;  APPLICANT:  XU, Yuming
;  APPLICANT:  ARVIZU, Chandra S.
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  DING, Li
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  LU, Yan
;  APPLICANT:  YUE, Henry
;  APPLICANT:  BURFORD, Neil
;  APPLICANT:  BANDMAN, Olga
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  LAL, Preeti G.
;  APPLICANT:  RECIPON, Shirley A.
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  BOROWSKY, Mark L.
;  APPLICANT:  THORNTON, Michael B.
;  APPLICANT:  SWARNAKER Anita
;  APPLICANT:  THANGAVELU, Kavitha
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  ISON, Craig H.
;  TITLE OF INVENTION: HUMAN KINASES
;  FILE REFERENCE: PI-0262 USN
;  CURRENT APPLICATION NUMBER: US/10/415,011
;  CURRENT FILING DATE:  2003-04-18
;  PRIOR APPLICATION NUMBER: PCT/US01/47728
;  PRIOR FILING DATE: 2001-10-20
;  PRIOR APPLICATION NUMBER: US 60/242,410
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/244,068
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: US 60/245,708
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: US 60/247,672
;  PRIOR FILING DATE: 2000-11-09
;  PRIOR APPLICATION NUMBER: US 60/249,565
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: US 60/252,730
;  PRIOR FILING DATE: 2000-11-22
;  PRIOR APPLICATION NUMBER: US 60/250,807
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PERL Program
; SEQ ID NO 12
;   LENGTH: 485
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040053394A1 7473788CD1
US-10-415-011-12

  Query Match             91.3%;  Score 337;  DB 4;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-307;
  Matches  337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPA 337
              |||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPA 454


RESULT 10
US-10-168-582-12
; Sequence 12, Application US/10168582
; Publication No. US20040058426A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  YANG, Junming
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  BURFORD, Neil
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  REDDY, Roopa
;  APPLICANT:  YUE, Henry
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  KAHN, Farrah A.
;  TITLE OF INVENTION: HUMAN KINASES
;  FILE REFERENCE: PI-0002 PCT
;  CURRENT APPLICATION NUMBER: US/10/168,582
;  CURRENT FILING DATE:  2002-06-20
;  PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731
;  PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PERL Program
; SEQ ID NO 12
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040058426A1 3244919CD1
US-10-168-582-12

  Query Match             81.3%;  Score 300;  DB 4;  Length 375;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-272;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350


RESULT 11
US-10-074-978A-161
; Sequence 161, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 161
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-074-978A-161

  Query Match            56.6%;  Score 209;  DB 4;  Length 255;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-187;
  Matches  209;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 86

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 146

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 206

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMV 209
              |||||||||||||||||||||||||||||
Db        207 HSSNAVESLVQLFSTVSVQYVPTWSKEMV 235


RESULT 12
US-10-074-978A-159
; Sequence 159, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
```

```
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-074-978A-159

  Query Match             56.6%;  Score 209;  DB 4;  Length 258;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-187;
  Matches  209;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 86

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 146

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 206

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMV 209
              |||||||||||||||||||||||||||||
Db        207 HSSNAVESLVQLFSTVSVQYVPTWSKEMV 235


RESULT 13
US-10-074-978A-18
; Sequence 18, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 488
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-074-978A-18

  Query Match             56.6%;  Score 209;  DB 4;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-187;
  Matches  209;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 178

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 238

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 298

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMV 209
              |||||||||||||||||||||||||||||
Db        299 HSSNAVESLVQLFSTVSVQYVPTWSKEMV 327


RESULT 14
US-10-074-978A-163
; Sequence 163, Application US/10074978A
; Publication No. US20040010119A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-074-978A-163

  Query Match            51.8%;  Score 191;  DB 4;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 2e-170;
  Matches  191;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 84

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 144

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 204

Qy        181 HSSNAVESLVQ 191
              ||||||||||| 
Db        205 HSSNAVESLVQ 215


RESULT 15
US-09-801-876B-6
; Sequence 6, Application US/09801876B
; Patent No. US20020127683A1
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160
;  CURRENT APPLICATION NUMBER: US/09/801,876B
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-09-801-876B-6

  Query Match            30.6%;  Score 113;  DB 3;  Length 384;
  Best Local Similarity  100.0%;  Pred. No. 4.6e-97;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        111 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GHAHLTDFNIATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYE 212

Qy        171 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 LLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR 265


Search completed: May  9, 2006, 10:51:50
Job time : 49 secs
```

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:50:58 ; Search time 27 Seconds
(without alignments)
632.558 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 369
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 235405 seqs, 46284737 residues

Word size : 1

Total number of hits satisfying chosen parameters: 235171

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep1:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep1:*
8: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
9: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep1:*
10: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
11: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep1:*
12: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	300	81.3	375	9	US-10-979-095-12	Sequence 12, Appl
2	35	9.5	225	11	US-11-125-295-5	Sequence 5, Appli
3	35	9.5	236	11	US-11-125-295-7	Sequence 7, Appli
4	35	9.5	364	9	US-10-194-487-572	Sequence 572, App
5	35	9.5	364	9	US-10-195-883-572	Sequence 572, App
6	35	9.5	364	9	US-10-195-888-572	Sequence 572, App
7	35	9.5	364	9	US-10-195-889-572	Sequence 572, App
8	35	9.5	396	11	US-11-125-295-11	Sequence 11, Appl
9	35	9.5	407	11	US-11-125-295-9	Sequence 9, Appli
10	9	2.4	1388	9	US-10-501-035-350	Sequence 350, App
11	8	2.2	256	11	US-11-096-568A-23243	Sequence 23243, A
12	8	2.2	283	9	US-10-506-454-365	Sequence 365, App
13	8	2.2	346	11	US-11-000-365-52	Sequence 52, Appl
14	8	2.2	346	11	US-11-032-794-52	Sequence 52, Appl
15	8	2.2	370	11	US-11-096-568A-23242	Sequence 23242, A
16	8	2.2	377	11	US-11-096-568A-23241	Sequence 23241, A
17	8	2.2	401	11	US-11-000-365-50	Sequence 50, Appl
18	8	2.2	401	11	US-11-032-794-50	Sequence 50, Appl
19	8	2.2	550	11	US-11-113-837-17	Sequence 17, Appl
20	8	2.2	561	11	US-11-090-617-562	Sequence 562, App
21	8	2.2	598	11	US-11-113-837-18	Sequence 18, Appl
22	8	2.2	605	11	US-11-087-099-3240	Sequence 3240, Ap
23	8	2.2	635	11	US-11-113-837-16	Sequence 16, Appl
24	8	2.2	637	11	US-11-113-837-4	Sequence 4, Appli
25	8	2.2	637	11	US-11-087-099-866	Sequence 866, App
26	8	2.2	639	11	US-11-113-837-21	Sequence 21, Appl
27	8	2.2	665	11	US-11-113-837-19	Sequence 19, Appl
28	8	2.2	665	11	US-11-087-099-10870	Sequence 10870, A
29	8	2.2	668	11	US-11-111-239-13	Sequence 13, Appl
30	8	2.2	683	11	US-11-087-099-4971	Sequence 4971, Ap
31	8	2.2	683	11	US-11-087-099-7461	Sequence 7461, Ap
32	8	2.2	683	11	US-11-188-298-17476	Sequence 17476, A
33	8	2.2	1197	9	US-10-055-877-8	Sequence 8, Appli
34	8	2.2	1247	9	US-10-055-877-10	Sequence 10, Appl
35	8	2.2	1372	11	US-11-087-099-3054	Sequence 3054, Ap
36	8	2.2	1372	11	US-11-188-298-13921	Sequence 13921, A
37	8	2.2	1590	9	US-10-055-877-146	Sequence 146, App
38	7	1.9	36	11	US-11-224-106-1	Sequence 1, Appli
39	7	1.9	168	11	US-11-096-568A-11681	Sequence 11681, A
40	7	1.9	169	11	US-11-096-568A-24880	Sequence 24880, A
41	7	1.9	173	11	US-11-096-568A-24879	Sequence 24879, A
42	7	1.9	183	11	US-11-096-568A-14295	Sequence 14295, A
43	7	1.9	193	8	US-10-511-937-2441	Sequence 2441, Ap
44	7	1.9	193	11	US-11-224-106-4	Sequence 4, Appli
45	7	1.9	193	11	US-11-224-106-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-979-095-12
; Sequence 12, Application US/10979095
; Publication No. US20060068481A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; APPLICANT: KAHN, Farrah A.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0002 PCT
; CURRENT APPLICATION NUMBER: US/10/979,095
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/10/168,582
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 3244919CD1
US-10-979-095-12

Query Match 81.3%; Score 300; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.5e-288;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350


RESULT 2
US-11-125-295-5
; Sequence 5, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/11/125,295
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US/10/620,845
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-125-295-5

  Query Match             9.5%;  Score 35;  DB 11;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-26;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
                ||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 3
US-11-125-295-7
; Sequence 7, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/11/125,295
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US/10/620,845
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-125-295-7

  Query Match             9.5%;  Score 35;  DB 11;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-26;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
                ||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 4
US-10-194-487-572
; Sequence 572, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C312
;  CURRENT APPLICATION NUMBER: US/10/194,487
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-194-487-572

  Query Match             9.5%;  Score 35;  DB 9;  Length 364;
```

Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         32 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 66
```

RESULT 5
US-10-195-883-572
; Sequence 572, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C323
; CURRENT APPLICATION NUMBER: US/10/195,883
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-883-572

Query Match 9.5%; Score 35; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         32 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 66
```

RESULT 6
US-10-195-888-572
; Sequence 572, Application US/10195888
; Publication No. US20060073545A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C324
; CURRENT APPLICATION NUMBER: US/10/195,888
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-888-572

Query Match 9.5%; Score 35; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         32 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 66
```

RESULT 7
US-10-195-889-572
; Sequence 572, Application US/10195889
; Publication No. US20060074227A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C329
; CURRENT APPLICATION NUMBER: US/10/195,889
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-889-572

Query Match 9.5%; Score 35; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         32 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 66
```

RESULT 8
US-11-125-295-11
; Sequence 11, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/11/125,295
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US/10/620,845
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-125-295-11

  Query Match             9.5%;  Score 35;  DB 11;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 2e-26;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 9
US-11-125-295-9
; Sequence 9, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/11/125,295
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US/10/620,845
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 407
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-125-295-9

  Query Match             9.5%;  Score 35;  DB 11;  Length 407;
  Best Local Similarity   100.0%;  Pred. No. 2e-26;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 69
              |||||||||||||||||||||||||||||||||||
Db         82 FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV 116


RESULT 10
US-10-501-035-350
; Sequence 350, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
;  TITLE OF INVENTION:  ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
;  TITLE OF INVENTION:  AND/OR PROTEIN TYROSINE KINASE PATHWAYS
;  FILE REFERENCE: D0185 PCT
;  CURRENT APPLICATION NUMBER: US/10/501,035
;  CURRENT FILING DATE:  2004-07-09
;  PRIOR APPLICATION NUMBER: US 60/350,061
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 795
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 350
;   LENGTH: 1388
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-501-035-350

  Query Match             2.4%;  Score 9;  DB 9;  Length 1388;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         96 IHRDVKPDN 104
              |||||||||
Db        211 IHRDVKPDN 219


RESULT 11
US-11-096-568A-23243
; Sequence 23243, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23243
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(256)
;   OTHER INFORMATION: Ceres Seq. ID no. 12411724
US-11-096-568A-23243

  Query Match             2.2%;  Score 8;  DB 11;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 6.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         94 HIIHRDVK 101
              ||||||||
Db         46 HIIHRDVK 53


RESULT 12
US-10-506-454-365
; Sequence 365, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
;  APPLICANT: Slesarev, Alexi I
;  APPLICANT:  Mezhevaya, Katja V
;  APPLICANT:  Polushin, Nikolai N
;  APPLICANT:  Shcherbinina, Olga V
;  APPLICANT:  Shakhova, Vera V
;  APPLICANT:  Malykh, Andrei G
;  APPLICANT:  Kozyavkin, Sergei A
;  TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
;  TITLE OF INVENTION:  Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogens
;  TITLE OF INVENTION:  and Methods of Use Thereof
;  FILE REFERENCE: FID001
;  CURRENT APPLICATION NUMBER: US/10/506,454
;  CURRENT FILING DATE:  2004-08-31
;  PRIOR APPLICATION NUMBER: PCT/US03/06664
;  PRIOR FILING DATE: 2003-03-04
;  PRIOR APPLICATION NUMBER: 60/361,742
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 1722
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 365
;   LENGTH: 283
;   TYPE: PRT
;   ORGANISM: Methanopyrus kandleri
```

US-10-506-454-365

Query Match 2.2%; Score 8; DB 9; Length 283;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        254 VPNKGRLH 261
              ||||||||
Db          6 VPNKGRLH 13
```

RESULT 13
US-11-000-365-52
; Sequence 52, Application US/11000365
; Publication No. US20050267022A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BUBICI, CONCETTA
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
; TITLE OF INVENTION: CELL DEATH OR APOPTOSIS BY TARGETING JNK
; FILE REFERENCE: 21459-97705
; CURRENT APPLICATION NUMBER: US/11/000,365
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-000-365-52

Query Match 2.2%; Score 8; DB 11; Length 346;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        104 NILLDERG 111
              ||||||||
Db        175 NILLDERG 182
```

RESULT 14
US-11-032-794-52
; Sequence 52, Application US/11032794
; Publication No. US20050265970A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BUBICI, CONCETTA
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
; TITLE OF INVENTION: CELL DEATH OR APOPTOSIS BY TARGETING JNK
; FILE REFERENCE: 21459-97816
; CURRENT APPLICATION NUMBER: US/11/032,794
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 11/000,365
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-032-794-52

Query Match 2.2%; Score 8; DB 11; Length 346;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        104 NILLDERG 111
              ||||||||
Db        175 NILLDERG 182
```

RESULT 15
US-11-096-568A-23242
; Sequence 23242, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23242
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(370)
; OTHER INFORMATION: Ceres Seq. ID no. 12411723
US-11-096-568A-23242

Query Match 2.2%; Score 8; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         94 HIIHRDVK 101
              ||||||||
Db        160 HIIHRDVK 167
```

Search completed: May 9, 2006, 10:55:12
Job time : 28 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:45:32 ; Search time 40 Seconds
(without alignments)
887.600 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 1942
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	754	38.8	379	2	T23688	hypothetical prote
2	458	23.6	733	2	A57459	ribosomal protein
3	453	23.3	380	1	OKBYC2	protein kinase (EC
4	445	22.9	479	2	A38578	protein kinase 2 (
5	445	22.9	752	1	A32571	ribosomal protein
6	444	22.9	740	2	I38556	ribosomal protein
7	439	22.6	733	1	B30001	ribosomal protein
8	434.5	22.4	465	2	S68462	protein kinase ATP
9	432	22.2	648	1	JQ1150	protein kinase (EC
10	429.5	22.1	646	2	T38171	probable serine/th
11	429	22.1	735	2	I51901	ribosomal protein
12	428	22.0	471	2	S68463	protein kinase ATP
13	427	22.0	629	2	A30001	ribosomal protein
14	427	22.0	735	2	A53300	ribosomal protein
15	425.5	21.9	823	2	S48986	probable protein k
16	424	21.8	586	2	A53758	protein kinase C (
17	424	21.8	587	2	A49509	protein kinase C (
18	423	21.8	480	2	S56639	ribosomal protein
19	423	21.8	633	2	C32571	ribosomal protein
20	421.5	21.7	696	2	S55694	protein kinase (EC
21	419	21.6	398	1	OKBYC3	protein kinase (EC
22	417.5	21.5	425	2	S41099	protein kinase (EC
23	416	21.4	351	1	OKHYCB	protein kinase (EC
24	416	21.4	351	1	OKMSCB	protein kinase (EC
25	416	21.4	351	1	OKRTCB	protein kinase (EC
26	416	21.4	480	1	A39360	protein kinase (EC
27	414	21.3	359	2	T21211	hypothetical prote
28	414	21.3	399	1	OKBYC1	protein kinase (EC
29	413	21.3	360	1	OKHUCG	protein kinase (EC
30	411.5	21.2	353	2	C31751	protein kinase (EC
31	409.5	21.1	351	1	OKMSCA	protein kinase (EC
32	409.5	21.1	352	2	S19027	protein kinase A (
33	409	21.1	338	2	T41021	ser-thr protein ki
34	408.5	21.0	334	2	A60543	protein kinase (EC
35	408.5	21.0	352	2	S19028	protein kinase (EC
36	408	21.0	351	1	OKBOB1	protein kinase (EC
37	408	21.0	351	1	OKHUCB	protein kinase (EC
38	408	21.0	397	1	OKBOB2	protein kinase (EC
39	407.5	21.0	302	2	PC4287	protein kinase (EC
40	407.5	21.0	351	1	OKBO2C	protein kinase (EC
41	407.5	21.0	351	1	OKHU2C	protein kinase (EC
42	407.5	21.0	351	1	OKHYCA	protein kinase (EC
43	407.5	21.0	351	1	OKRT2C	protein kinase (EC
44	407	21.0	338	2	S00085	protein kinase (EC
45	407	21.0	359	1	OKKWC1	protein kinase (EC

ALIGNMENTS

RESULT 1
T23688
hypothetical protein M03C11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23688
R;McMurray, A.
submitted to the EMBL Data Library, April 1995
A;Reference number: Z19783
A;Accession: T23688
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-379 <WIL>
A;Cross-references: UNIPROT:Q21483; UNIPARC:UPI000007B6C1; EMBL:Z49128; PIDN:CAA88953.1;
A;Experimental source: clone M03C11
C;Genetics:
A;Gene: CESP:M03C11.1
A;Map position: 3
A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 38.8%; Score 754; DB 2; Length 379;
Best Local Similarity 43.2%; Pred. No. 1.6e-29;
Matches 140; Conservative 70; Mismatches 106; Indels 8; Gaps 2;

```
Qy          2 YAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDL 61
              :|:|||||::|||:    || ||| :| :: | |:|||||:||| : |:|| ||||||||
Db         54 FALKYMNKRRCIEKGVAANVIRELTLLSKMSHPFIVNLWYTFQDGDYMYMVSDLLLGGDL 113

Qy         62 RYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIA 121
              |||| |  :|:||  :||:||: ||::||    |:|||:||:|||||:||||||| |:|
Db        114 RYHLSQQGKFAEDRAKLYLCEICLAVEYLHEMKIVHRDIKPENILLDEQGHAHLTDLNLA 173

Qy        122 TIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIH 181
              | ::| : ||: :||:|||||||: :::    ||   ||||::||  ||:|||  |::
Db        174 TQLEDDQLATSYSGTRPYMAPEIYATYLEIEDGYDSRVDWWALGVCFYEMLRGRTPFEFS 233

Qy        182 SSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLW 241
              |    |     |   |: |   | ::: : :| : | ||  |: ::       : :
Db        234 SRTKPEEAYVAFRESSIPYPAHWPTDLIQFINSMLKFDKEKRLVGLEAIKKHSYTERIDF 293

Qy        242 DHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSE 301
              : ||:  | |:| |  |:||| :|||| || | |:|:::     | :  : | ||: :
Db        294 KSVFEKKPSPVFIPCKEGLNCDPMYELEERILVSTPIHRRR----TNHNNSSGRSSSEPQ 349

Qy        302 NDYLQDCLDAIQQDFVIFNREKLK 325
              |  | :    : : |: |:|  :|
Db        350 NAALVE----VSKAFIDFSRHNVK 369
```

RESULT 2
A57459

ribosomal protein S6 kinase 2 (EC 2.7.1.-) 2 - human
N;Alternate names: growth factor-stimulated protein kinase (GFSPK); p90 S6 kinase; ribos
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57459; I64834
R;Zhao, Y.; Bjorbaek, C.; Weremowicz, S.; Morton, C.C.; Moller, D.E.
Mol. Cell. Biol. 15, 4353-4363, 1995
A;Title: RSK3 encodes a novel pp90rsk isoform with a unique N-terminal sequence: growth
A;Reference number: A57459; MUID:95349602; PMID:7623830
A;Accession: A57459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-733 <ZHA>
A;Cross-references: UNIPROT:Q15349; UNIPARC:UPI0000032EF7; EMBL:X85106; NID:g1033032; PI
R;Moller, D.E.; Xia, C.H.; Tang, W.; Zhu, A.X.; Jakubowski, M.
Am. J. Physiol. 266, 351-359, 1994
A;Title: Human rsk isoforms: cloning and characterization of tissue-specific expression.
A;Reference number: I51901
A;Accession: I64834
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'A',1-255,'A',257-268,'S',270-446,'G',448-539 <MOL>
A;Cross-references: UNIPARC:UPI000016AFE5; GB:L07598; NID:g401771; PIDN:AAC82496.1; PID:
C;Comment: Although ribosomal protein S6 (see PIR:R3HU6) is phosphorylated by this enzym
C;Genetics:
A;Gene: GDB:RPS6KA2; pp90RSK3; RSK; HU-2; RSK3
A;Cross-references: GDB:365645; OMIM:601685
A;Map position: 6q27-6q27
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
C;Keywords: ATP; autophosphorylation; monomer; phosphoprotein; phosphotransferase; serin
F;57-318/Domain: protein kinase homology <KIN1>
F;65-73/Region: protein kinase ATP-binding motif
F;413-672/Domain: protein kinase homology <KIN2>
F;421-429/Region: protein kinase ATP-binding motif

Query Match 23.6%; Score 458; DB 2; Length 733;
Best Local Similarity 37.5%; Pred. No. 4e-15;
Matches 103; Conservative 51; Mismatches 103; Indels 18; Gaps 6;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| : |     || ||:   | :|| |: | |:| | |:|| |  :::::| | |||
Db         87 LYAMKVLKKATLKVRDRVRSKM-ERDILAEVNHPFIVKLHYAFQTEGKLYLILDFLRGGD 145

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |   | : | |:|: |: |: |:|||||:|    ||:||:||:|||||| ||  :||| :
Db        146 LFTRLSKEVMFTEEDVKFYLAELALALDHLHSLGIIYRDLKPENILLDEEGHIKITDFGL 205

Qy        121 A-TIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              :   |   :|| :  ||  |||||: :       |::   |||| ||: :|:| |  |:
Db        206 SKEAIDHDKRAYSFCGTIEYMAPEVVNR-----RGHTQSADWWSFGVLMFEMLTGSLPFQ 260

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSS----LQDVQAAPA 235
                  :|:       |::   | |  :||| |   || :|| :    :::::  |
Db        261 GKDRKETMALILKAKLGMPQFL---SGEAQSLLRALFKRNPCNRLGAGIDGVEEIKRHPF 317

Qy        236 LAGVLWDHLSEKRVEPGFVPNKGR----LHCDPTF 266
                : |: |  | ::| | |  ||     | || |
Db        318 FVTIDWNTLYRKEIKPPFKPALGRPEDTFHFDPEF 352
```

RESULT 3
OKBYC2
protein kinase (EC 2.7.1.37), cAMP-dependent, catalytic chain 2 - yeast (Saccharomyces c
N;Alternate names: protein kinase YKR; protein P1855; protein YPL203w
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S65222; B27070; S00125
R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65202
A;Accession: S65222
A;Molecule type: DNA
A;Residues: 1-380 <RIE>
A;Cross-references: UNIPROT:P06245; UNIPARC:UPI0000052E94; EMBL:Z73559; NID:g1370421; PII
A;Experimental source: strain S288C (AB972)
R;Toda, T.; Cameron, S.; Sass, P.; Zoller, M.; Wigler, M.
Cell 50, 277-287, 1987
A;Title: Three different genes in S. cerevisiae encode the catalytic subunits of the cAMI
A;Reference number: A90896; MUID:87244343; PMID:3036373
A;Accession: B27070
A;Molecule type: DNA
A;Residues: 1-288,'Q',290-380 <TOD>
A;Cross-references: UNIPARC:UPI0000168E99; EMBL:M17073; NID:g173010; PIDN:AAA35165.1; PII
R;Ohno, S.; Aoshima, M.; Matsumoto, S.; Yahara, I.; Suzuki, K.
FEBS Lett. 222, 279-285, 1987
A;Title: A yeast gene coding for a putative protein kinase homologous to cdc25 suppressir
A;Reference number: S00125; MUID:88005168; PMID:3308514
A;Accession: S00125
A;Molecule type: DNA
A;Residues: 1-213,'LRQRGTN',221-259,'V',261-380 <OHN>
A;Cross-references: UNIPARC:UPI0000168E98; EMBL:Y00694; NID:g4624; PIDN:CAA68689.1; PID:g
C;Genetics:
A;Gene: SGD:TPK2; TPK2; YKR1; PKA2; MIPS:YPL203w
A;Cross-references: SGD:S0006124
A;Map position: 16L
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; cAMP binding; heterotetramer; magnesium; phosphoprotein; phosphotransfer
F;2-380/Product: protein kinase, cAMP-dependent, catalytic chain 2 #status predicted <MA1
F;68-324/Domain: protein kinase homology <KIN>
F;76-84/Region: protein kinase ATP-binding motif
F;81,82,148,154,197,210/Binding site: Mg-ATP (Phe, Gly, Asp, Glu, Glu, Thr) #status predi
F;99,118,193,195/Active site: Lys, Glu, Asp, Lys #status predicted
F;198,211/Binding site: magnesium (Asn, Asp) #status predicted
F;224/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 23.3%; Score 453; DB 1; Length 380;
Best Local Similarity 37.3%; Pred. No. 3.7e-15;
Matches 97; Conservative 55; Mismatches 90; Indels 18; Gaps 6;

```
Qy          2 YAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDL 61
              ||:| : ||| ::  :| :   |  :|: :|| ||: :| :|||  ::|||:| : ||:|
Db         96 YAIKVLKKQQVVKMKQVEHTNDERRMLKLVEHPFLIRMWGTFQDARNIFMVMDYIEGGEL 155

Qy         62 RYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIA 121
                 |::: :|     : |  |: |||:||   :||:||:||:|||||  ||  :|||  |
Db        156 FSLLRKSQRFPNPVAKFYAAEVILALEYLHAHNIIYRDLKPENILLDRNGHIKITDFGFA 215

Qy        122 TIIKDGERAT-ALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRP-YD 179
                |: :  |  | ||  |:|||:  :       |:  |||||:||: ||:| |: | ||
Db        216 ---KEVQTVTWTLCGTPDYIAPEVITT-----KPYNKSVDWWSLGVLIYEMLAGYTPFYD 267

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQ----DVQAAPA 235
                    | ::|      | | | :  ::| || ||:| :   |: :||    |::| |
Db        268 TTPMKTYEKILQ----GKVVYPPYFHPDVVDLLSKLITADLTRRIGNLQSGSRDIKAHPW 323

Qy        236 LAGVLWDHLSEKRVEPGFVP 255
               : |:|: |  | :|  : |
Db        324 FSEVVWERLLAKDIETPYEP 343
```

RESULT 4
A38578
protein kinase 2 (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 31-Dec-2004
C;Accession: A38578
R;Haribabu, B.; Dottin, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum
A;Reference number: A38578; MUID:91142122; PMID:1996312
A;Accession: A38578
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-479 <HAR>
A;Cross-references: UNIPROT:P28178; UNIPARC:UPI0000131B58; GB:M59744; NID:g167717; PIDN:A
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonir

```
F;151-407/Domain: protein kinase homology <KIN>
F;159-167/Region: protein kinase ATP-binding motif

  Query Match             22.9%;  Score 445;  DB 2;  Length 479;
  Best Local Similarity   33.6%;  Pred. No. 1.1e-14;
  Matches  108;  Conservative   63;  Mismatches  116;  Indels   34;  Gaps    9;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ::||| : |    | | :| :   |  ||| | | |:||| |:|| :: ::||:| : ||:
Db        178 IFAMKVLRKDAIIARKQVNHTKSEKTILQCISHPFIVNLHYAFQTKDKLYMVLDFVNGGE 237

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              | :||::  :|||  |::|  |:  |||:|  | |::||:|:|||||  ||  :||| :
Db        238 LFFHLKREGRFSEPRVKIYAAEIVSALDHLHKQDIVYRDLKPENILLDSEGHICITDFGL 297

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              :  |:  :       ||  |:|||: :     | |:   |||||:| : ||:| |  |:
Db        298 SKKIETTDGTFTFCGTPEYLAPEVLN-----GHGHGCAVDWWSLGTLLYEMLTGLPPF-- 350

Qy        181 HSSNAVESLVQLFSTVSVQY---------VPTW-SKEMVALLRKLLTVNPEHRLSSL--Q 228
              :| |           || |         :||: | |  :||  |||   : || :
Db        351 YSQN-----------VSTMYQKILNGELKIPTYISPEAKSLLEGLLTREVDKRLGTKGGG 399

Qy        229 DVQAAPALAGVLWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKN 288
              :|:  |    : |: |  | ||  | | | :   | : ::: :  : ||:    :  |
Db        400 EVKQHPWFKNIDWEKLDRKEVEVHFKP-KVKSGTDIS-QIDPVFTQERPMDSLVETSALG 457

Qy        289 KSRDNSRDSSQSENDYLQDCL 309
               :   :|:|     |: | :
Db        458 DAM--GKDTSFEGFTYVADSI 476


RESULT 5
A32571
ribosomal protein S6 kinase II (EC 2.7.1.-) alpha chain homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A32571
R;Alcorta, D.A.; Crews, C.M.; Sweet, L.J.; Bankston, L.; Jones, S.W.; Erikson, R.L.
Mol. Cell. Biol. 9, 3850-3859, 1989
A;Title: Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis ri
A;Reference number: A93113; MUID:89384612; PMID:2779569
A;Accession: A32571
A;Molecule type: mRNA
A;Residues: 1-752 <ALC>
A;Cross-references: UNIPROT:P18652; UNIPARC:UPI000012DB30; GB:M28488; NID:g551555; PIDN:
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;78-339/Domain: protein kinase homology <KIN1>
F;86-94/Region: protein kinase ATP-binding motif
F;433-692/Domain: protein kinase homology <KIN2>

  Query Match             22.9%;  Score 445;  DB 1;  Length 752;
  Best Local Similarity   36.2%;  Pred. No. 1.7e-14;
  Matches  102;  Conservative   51;  Mismatches  113;  Indels   16;  Gaps    6;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| : |     || ||    | :|| :: | |:| | |:|| |  :::::| | |||
Db        108 LYAMKVLKKATLKVRDRVRTKI-ERDILADVNHPFVVKLHYAFQTEGKLYLILDFLRGGD 166

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |    | : | |:|: |: |: |:|| ||:|    ||:||:||:|||||| ||  |||| :
Db        167 LFTRLSKEVMFTEEDVKFYLAELALGLDHLHSLGIIYRDLKPENILLDEEGHIKLTDFGL 226

Qy        121 ATIIKDGE-RATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              :    | | :| :  ||  |||||: :       |:|   |||| ||: :|:| |  |:
Db        227 SKEAIDHEKKAYSFCGTVEYMAPEVVNR-----QGHSHSADWWSYGVLMFEMLTGSLPFQ 281

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSS----LQDVQAAPA 235
                  :|:       |::   | |  :||| |   || :|| |     :::: |
Db        282 GKDRKETMTLILKAKLGMPQFL---SAEAQSLLRALFKRNPANRLGSGPDGAEEIKRHPF 338

Qy        236 LAGVLWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRP 277
                : : |: |  : ::| | |  |:   | ||  :       |
Db        339 YSTIDWNKLYRREIKPPFKPAVGQ--PDDTFYFDTEFTSRTP 378


RESULT 6
I38556
ribosomal protein S6 kinase 2 (EC 2.7.1.-) 3 - human
N;Alternate names: insulin-stimulated protein kinase 1 (PK-1, ISPK1); MAP kinase-activat
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: I38556; I64835
R;Bjorbaek, C.; Vik, T.A.; Echwald, S.M.; Webb, G.C.; Wang, J.P.; Yang, P.Y.; Vestergaar
Diabetes 44, 90-97, 1995
A;Title: Cloning of a human insulin-stimulated protein kinase (ISPK-1) gene and analysis
nts.
A;Reference number: I38556; MUID:95113220; PMID:7813820
A;Accession: I38556
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-740 <BJO>
A;Cross-references: UNIPROT:P51812; UNIPARC:UPI000012DB2E; EMBL:U08316; NID:g475587; PID
R;Moller, D.E.; Xia, C.H.; Tang, W.; Zhu, A.X.; Jakubowski, M.
Am. J. Physiol. 266, 351-359, 1994
A;Title: Human rsk isoforms: cloning and characterization of tissue-specific expression.
A;Reference number: I51901
A;Accession: I64835
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 2-423,'L',425-479,'N',481-493,495-582 <MOL>
A;Cross-references: UNIPARC:UPI000016AFE6; GB:L07599; GB:L07601; NID:g401773; PIDN:AAC82
C;Comment: Although ribosomal protein S6 (see PIR:R3HU6) is phosphorylated by this enzym
C;Genetics:
A;Gene: GDB:RPS6KA3; RSK; HU-2; RSK2; HU-3
A;Cross-references: GDB:365648; OMIM:300075
A;Map position: Xp22.2-Xp22.2
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
C;Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific
F;66-327/Domain: protein kinase homology <KIN1>
F;74-82/Region: protein kinase ATP-binding motif
F;420-679/Domain: protein kinase homology <KIN2>
F;428-436/Region: protein kinase ATP-binding motif

  Query Match             22.9%;  Score 444;  DB 2;  Length 740;
  Best Local Similarity   36.4%;  Pred. No. 1.9e-14;
  Matches  100;  Conservative   52;  Mismatches  105;  Indels   18;  Gaps    6;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| : |     || ||    | :|| |: | |:| | |:|| |  :::::| | |||
Db         96 LYAMKVLKKATLKVRDRVRTKM-ERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGD 154

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |    | : | |:|: |: |: |:|||||:|    ||:||:||:|||||| ||  |||| :
Db        155 LFTRLSKEVMFTEEDVKFYLAELALALDHLHSLGIIYRDLKPENILLDEEGHIKLTDFGL 214

Qy        121 ATIIKDGE-RATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              :    | | :| :  ||  |||||: :       |::   |||| ||: :|:| |  |:
Db        215 SKESIDHEKKAYSFCGTVEYMAPEVVNR-----RGHTQSADWWSFGVLMFEMLTGTLPFQ 269

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSS----LQDVQAAPA 235
                  :::       |::   | |  :||| |   || :|| |     :::: |
Db        270 GKDRKETMTMILKAKLGMPQFL---SPEAQSLLRMLFKRNPANRLGAGPDGVEEIKRHSF 326

Qy        236 LAGVLWDHLSEKRVEPGFVPNKGR----LHCDPTF 266
                : : |: |  : : | | |  ||      : || |
Db        327 FSTIDWNKLYRREIHPPFKPATGRPEDTFYFDPEF 361


RESULT 7
B30001
ribosomal protein S6 kinase (EC 2.7.1.-) II alpha chain - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: B30001
```

```
R;Jones, S.W.; Erikson, E.; Blenis, J.; Maller, J.L.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 3377-3381, 1988
A;Title: A Xenopus ribosomal protein S6 kinase has two apparent kinase domains that are
A;Reference number: A30001; MUID:88217904; PMID:3368449
A;Accession: B30001
A;Molecule type: mRNA
A;Residues: 1-733 <JON>
A;Cross-references: UNIPROT:P10665; UNIPARC:UPI000012DB31; GB:M20187; NID:g214786; PIDN:
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;60-321/Domain: protein kinase homology <KIN1>
F;68-76/Region: protein kinase ATP-binding motif
F;414-673/Domain: protein kinase homology <KIN2>
F;422-430/Region: protein kinase ATP-binding motif #status atypical

  Query Match            22.6%;  Score 439;  DB 1;  Length 733;
  Best Local Similarity  37.3%;  Pred. No. 3.2e-14;
  Matches   97;  Conservative   48;  Mismatches  101;  Indels   14;  Gaps    5;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| : |     || ||    | :|| :: | |:| | |:|| |  :::::| | |||
Db         90 LYAMKVLKKATLKVRDRVRTKM-ERDILADVHHPFVVRLHYAFQTEGKLYLILDFLRGGD 148

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |   | : | |:|: |: |: |:|| ||:|    ||:||:||:|||||| ||  |||| :
Db        149 LFTRLSKEVMFTEEDVKFYLAELALGLDHLHSLGIIYRDLKPENILLDEEGHIKLTDFGL 208

Qy        121 ATIIKDGE-RATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              :    | | :| :  ||  |||||: :       |:|   |||| ||: :|:| |  |:
Db        209 SKEAIDHEKKAYSFCGTVEYMAPEVVNR-----QGHSHSADWWSYGVLMFEMLTGSLPFQ 263

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSS----LQDVQAAPA 235
                      :|:        |::   | |  :||| |   || :|| |     ::::  |
Db        264 GKDRKETMTLILKAKLGMPQFL---SNEAQSLLRALFKRNPTNRLGSAMEGAEEIKRQPF 320

Qy        236 LAGVLWDHLSEKRVEPGFVP 255
                : : |: |  : : | | |
Db        321 FSTIDWNKLFRREMSPPFKP 340


RESULT 8
S68462
protein kinase ATPK6/ATPK1 (EC 2.7.1.-) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
C;Accession: S68462; A54141
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A;Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
A;Reference number: S68462; MUID:95129712; PMID:7828736
A;Accession: S68462
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-465 <MIZ>
A;Cross-references: UNIPROT:P42818; UNIPARC:UPI000000178F; EMBL:D42056; NID:g867996; PID
R;Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
J. Biol. Chem. 269, 17586-17592, 1994
A;Title: atpk1, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation, ch
A;Reference number: A54141; MUID:94292519; PMID:7912697
A;Contents: ecotype Landsberg erecta
A;Accession: A54141
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-465 <ZHA>
A;Cross-references: UNIPARC:UPI000000178F; GB:L29030; NID:g508307; PIDN:AAA21142.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:149344, NCBIP:149415)
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;132-389/Domain: protein kinase homology <KIN>
F;140-148/Region: protein kinase ATP-binding motif

  Query Match            22.4%;  Score 434.5;  DB 2;  Length 465;
  Best Local Similarity  34.7%;  Pred. No. 3.4e-14;
  Matches   94;  Conservative   51;  Mismatches  113;  Indels   13;  Gaps    4;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| | |   :|::    :  | :|| :|:| |:| | |||| :  :::|:| : ||
Db        159 IYAMKVMRKDHIMEKNHAEYMKAERDILTKIDHPFIVQLKYSFQTKYRLYLVLDFINGGH 218

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              | : |     | ||  |:|  |:  |: :|  : |:|||:||:|||:|  ||  |||| :
Db        219 LFFQLYHQGLFREDLARVYTAEIVSAVSHLHEKGIMHRDLKPENILMDTDGHVMLTDFGL 278

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |   ::  |: :: ||  ||||||       | |:    ||||||:: ||:| |  |: :
Db        279 AKEFEENTRSNSMCGTTEYMAPEIVR-----GKGHDKAADWWSVGILLYEMLTGKPPF-L 332

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHR----LSSLQDVQAAPAL 236
              |   ::  :        |::   | |  |:|: ||   || |    ||  ::::
Db        333 GSKGKIQQKIVKDKIKLPQFL---SNEAHAILKGLLQKEPERRLGSGLSGAEEIKQHKWF 389

Qy        237 AGVLWDHLSEKRVEPGFVPNKGRLHCDPTFE 267
              |: |  |  : | | | |       |   |:
Db        390 KGINWKKLEAREVMPSFKPEVSGRQCIANFD 420


RESULT 9
JQ1150
protein kinase (EC 2.7.1.37) cAMP-dependent, catalytic chain - slime mold (Dictyostelium
C;Species: Dictyostelium discoideum
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JQ1150
R;Buerki, E.; Anjard, C.; Scholder, J.C.; Reymond, C.D.
Gene 102, 57-65, 1991
A;Title: Isolation of two genes encoding putative protein kinases regulated during Dictyo
A;Reference number: JQ1150; MUID:91323730; PMID:1864510
A;Accession: JQ1150
A;Molecule type: DNA
A;Residues: 1-648 <BUE>
A;Cross-references: UNIPROT:P34099; UNIPARC:UPI000012DC1F; GB:M38703
C;Genetics:
A;Gene: PK2
A;Introns: 578/3
C;Complex: heterodimer with regulatory chain; active catalytic chain is released when cA
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Note: important for cell type differentiation and fruiting body morphogenesis
C;Superfamily: Dictyostelium cAMP-dependent protein kinase catalytic chain; protein kinas
C;Keywords: ATP; magnesium; phosphoprotein; phosphotransferase; serine/threonine-specific
F;126-223/Region: glutamine-rich
F;297-312/Region: glutamine-rich
F;334-590/Domain: protein kinase homology <KIN>
F;342-350/Region: protein kinase ATP-binding motif
F;365,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted
F;464,468/Binding site: magnesium (Asn, Asp) #status predicted

  Query Match            22.2%;  Score 432;  DB 1;  Length 648;
  Best Local Similarity  31.9%;  Pred. No. 6.2e-14;
  Matches   90;  Conservative   72;  Mismatches  104;  Indels   16;  Gaps    5;

Qy          2 YAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDL 61
              |||| :||   ::  :| ::  |  ||  | | |:|||: :||||: :::: : : ||::
Db        362 YAMKCLNKAYVVQLKQVEHLNSEKSILSSIHHPFIVNLYQAFQDEKKLYLLFEYVAGGEV 421

Qy         62 RYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIA 121
              ||:::::||  | : |  |: |||::|  |:|::||:||:|:|:| :||  :|||  |
Db        422 FTHLRKSMKFSNSTAKFYAAEIVLALEFLHKQNIVYRDLKPENLLIDNQGHIKITDFGFA 481

Qy        122 TIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIH 181
              ::|  |   | || |:|||| |      |:   ||||::|:: :|:| |: |:
Db        482 KRVED--RTFTLCGTPEYLAPEIIQS-----KGHGKAVDWWALGILIFEMLAGYPPFYDD 534

Qy        182 SSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQ----DVQAAPALA 237
              : |: : :       : :   :  :   |:::||| :   || :|:    ||:     :
Db        535 DTFAIYNKI---LAGRITFPLGFDVDAKDLIKRLLTADRTRRLGALKDGALDVKNHRWFS 591

Qy        238 GVLWDHLSEKRVEPGFVPNKGRLHCDPTFEL--EEMILESRP 277
```

```
                : |: | ::|    |:|          ||:  || ::|  |
Db        592 DINWERLYQRRDNGPFIPKIQHQGDSSNFEMYDEEEMVEEPP 633


RESULT 10
T38171
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - fission yeast (Schizosa
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C;Accession: T38171
R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z21775
A;Accession: T38171
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-646 <DEV>
A;Cross-references: UNIPROT:Q10364; UNIPARC:UPI000012DD14; EMBL:Z70043; NID:g1220275; PI
A;Experimental source: strain 972h-; cosmid c22E12
C;Genetics:
A;Gene: SPDB:SPAC22E12.14c
A;Map position: 1
C;Keywords: phosphotransferase; protein kinase

  Query Match             22.1%;  Score 429.5;  DB 2;  Length 646;
  Best Local Similarity   31.5%;  Pred. No. 8.2e-14;
  Matches  111;  Conservative   63;  Mismatches  123;  Indels   55;  Gaps   11;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQE---IEHVFLVNLWYSFQDEEDMFMVVDLLL 57
              :|||| ::|:  : | || :   | :|| :    :  |:| | :|||  :|:::| | :
Db        291 VYAMKVLSKKVIVRRKEVAHTVGERDILVQTSAADSPFIVALRFSFQTPKDLYLVTDYMA 350

Qy         58 GGDLRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTD 117
              ||:| :|||::|:| |:  : || |: |||  |  : |::||:||:|||:| :||  | |
Db        351 GGELFWHLQKSVRFPEERAKFYIAELLLALQALHKRGIVYRDLKPENILLDVQGHIALCD 410

Qy        118 FNIATI-IKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWR 176
              | ::   :  |       ||  |:|||:    :    ||   ||:||:|: ||:  ||
Db        411 FGLSKANLSVGTTTRTFCGTTDYLAPEV----ILDEAGYDMMVDFWSLGVLLYEMTCGWS 466

Qy        177 PYDIHSSNAVESLVQLFSTVSVQYV----PTWSKEMVALLRKLLTVNPEHRLSS---LQD 229
              |:          ::  ||:  :   |       | |   |:: ||  ||:||| :   :::
Db        467 PF------YADNTQQLYKNIVFGKVRFPRGLLSVEARDLIKLLLNRNPKHRLGAHGDVEE 520

Qy        230 VQAAPALAGVLWDHLSEKRVEPGFVP----------------NKGRLHCDPTFELEEMIL 273
              |   |   |: |  |: | : | | |                ||     |  |   : :
Db        521 VMKHPFFDGIDWKKLAAKEISPPFKPIVEGEIDVSNFDVEFTNKA---IDRDFSSTDEMS 577

Qy        274 ESRPLHKKKKRLAKN------KSRD------NSRDSS---QSENDYLQDCLD 310
              | ||    :   |        : |       || ||:    |::|| :|  |
Db        578 TSAPLSSTVQNGFKGFTYIDASAMDEAFGYHNSNDSASSISSQDDYSKDNSD 629


RESULT 11
I51901
ribosomal protein S6 kinase 2 (EC 2.7.1.-) 1 - human
N;Alternate names: MAP kinase-activated PK1; p90 S6 kinase; ribosomal protein S6 kinase
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I51901
R;Moller, D.E.; Xia, C.H.; Tang, W.; Zhu, A.X.; Jakubowski, M.
Am. J. Physiol. 266, 351-359, 1994
A;Title: Human rsk isoforms: cloning and characterization of tissue-specific expression.
A;Reference number: I51901
A;Accession: I51901
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-735 <MOL>
A;Cross-references: UNIPROT:Q15418; UNIPARC:UPI0000035BE4; GB:L07597; NID:g292456; PIDN:
C;Comment: Although ribosomal protein S6 (see PIR:R3HU6) is phosphorylated by this enzym
C;Genetics:
A;Gene: GDB:RPS6KA1; RSK; HU-1; RSK1
A;Cross-references: GDB:365638; OMIM:601684
A;Map position: 3pter-3qter
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
C;Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific
F;60-321/Domain: protein kinase homology <KIN1>
F;68-76/Region: protein kinase ATP-binding motif
F;416-675/Domain: protein kinase homology <KIN2>
F;424-432/Region: protein kinase ATP-binding motif

  Query Match             22.1%;  Score 429;  DB 2;  Length 735;
  Best Local Similarity   36.9%;  Pred. No. 9.8e-14;
  Matches   96;  Conservative   48;  Mismatches  102;  Indels   14;  Gaps    5;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| : |     || ||    | :|| :: | |:| | |:|| |  :::::| | |||
Db         90 LYAMKVLKKATLKVRDRVRTKM-ERDILADVNHPFVVKLHYAFQTEGKLYLILDFLRGGD 148

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |   | : | |:|: |: |: |:|| ||:|    ||:||:||:|||||| ||  |||| :
Db        149 LFTRLSKEVMFTEEDVKFYLAELALGLDHLHSLGIIYRDLKPENILLDEEGHIKLTDFGL 208

Qy        121 ATIIKDGE-RATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              :    | | :| :  ||  |||||: :       |:|   |||| ||: :|:| |  |:
Db        209 SKEAIDHEKKAYSFCGTVEYMAPEVVNR-----QGHSHSADWWSYGVLMFEMLTGSLPFQ 263

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSS----LQDVQAAPA 235
                    :|:        |:: |   |  :||| |   || :|| |     ::::
Db        264 GKDRKETMTLILKAKLGMPQFLST---EAQSLLRALFKRNPANRLGSGPDGAEEIKRHVF 320

Qy        236 LAGVLWDHLSEKRVEPGFVP 255
              : : |: |  : : | | |
Db        321 YSTIDWNKLYRREITPPFKP 340


RESULT 12
S68463
protein kinase ATPK19 (EC 2.7.1.-) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 05-Oct-2004
C;Accession: S68463
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A;Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
A;Reference number: S68462; MUID:95129712; PMID:7828736
A;Accession: S68463
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-471 <MIZ>
A;Cross-references: UNIPROT:Q39030; UNIPARC:UPI000016DAA6; EMBL:D42061; NID:g1526412; PI
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;138-395/Domain: protein kinase homology <KIN>
F;146-154/Region: protein kinase ATP-binding motif

  Query Match             22.0%;  Score 428;  DB 2;  Length 471;
  Best Local Similarity   31.7%;  Pred. No. 7.1e-14;
  Matches  100;  Conservative   54;  Mismatches  125;  Indels   36;  Gaps    6;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| | | : :|::    :  | :|| :|:| |:| | |||| :  :::|:| : ||
Db        165 IYAMKVMRKDKIVEKNHAEYMKAERDILTKIDHPFIVQLKYSFQTKYRLYLVLDFINGGH 224

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              | : |     | ||  |:|  |:   : :|  : |:|||:||:|||:|  ||  |||| :
Db        225 LFFQLYHQGLFREDLARVYTAEIVSVVSHLHEKGIMHRDLKPENILMDVDGHVMLTDFGL 284

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |    ::  |: :: ||  ||||||       | |:    ||||||:: ||:| |  |: :
Db        285 AKEFEENTRSNSMCGTTEYMAPEIVR-----GKGHDKAADWWSVGILLYEMLTGKPPF-L 338

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRL----SSLQDVQAAPAL 236
              |   ::  :        |:|     | |||: ||   || ||     |  ::::
Db        339 GSKGKIQQKIVKDKIKLPQFV---FNEAHALLKGLLQKEPERRLGSGPSGAEEIKKHKWF 395

Qy        237 AGVLWDHLSEKRVEPGFVPNKGRLHCDPTFE---LEEMILES---------------- 275
```

```
              : |  |  : |:| | |      |   |:    :  :|:|
Db        396 KAINWKKLEAREVQPSFKPAVSGRQCIANFDKCWTDMSVLDSPASSPNSDAKANPFTNFT 455

Qy        276 --RPLHKKKKRLAKN 288
                || |    |   |
Db        456 YVRPPHSFLHRTTSN 470


RESULT 13
A30001
ribosomal protein S6 kinase (EC 2.7.-.-) II beta chain - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A30001
R;Jones, S.W.; Erikson, E.; Blenis, J.; Maller, J.L.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 3377-3381, 1988
A;Title: A Xenopus ribosomal protein S6 kinase has two apparent kinase domains that are
A;Reference number: A30001; MUID:88217904; PMID:3368449
A;Accession: A30001
A;Molecule type: mRNA
A;Residues: 1-629 <JON>
A;Cross-references: UNIPROT:P10666; UNIPARC:UPI000012DB32; GB:M20188; NID:g214788; PIDN:
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;60-321/Domain: protein kinase homology <KIN1>
F;68-76/Region: protein kinase ATP-binding motif
F;414-629/Domain: protein kinase homology #status atypical <KIN2>
F;422-430/Region: protein kinase ATP-binding motif #status atypical

  Query Match             22.0%;  Score 427;  DB 2;  Length 629;
  Best Local Similarity   36.8%;  Pred. No. 1e-13;
  Matches   96;  Conservative   49;  Mismatches  102;  Indels   14;  Gaps    5;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| : |     || ||    | :|| :: | |:| | |:|| |  :::::| | |||
Db         90 LYAMKVLKKATLKVRDRVRTKM-ERDILADVHHPFVVRLHYAFQTEGKLYLILDFLRGGD 148

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |   | : | |:|: |: |: |:|| ||:|    ||:||:||:|||||| ||  |||| :
Db        149 LFTRLSKEVMFTEEDVKFYLAELALGLDHLHSLGIIYRDLKPENILLDEEGHIKLTDFGL 208

Qy        121 ATIIKDGE-RATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              :    | | :| :  ||  |||||: :       |:|   |||| ||: :|:| |  |:
Db        209 SKEAIDHEKKAYSFCGTVEYMAPEVVNR-----QGHSHGADWWSYGVLMFEMLTGSLPFQ 263

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSS----LQDVQAAPA 235
                 :|:       |::   | |  :||| |   |  :|| |     ::::  |
Db        264 GKDRKETMTLILKAKLGMPQFL---SNEAQSLLRALFKRNATNRLGSGVEGAEELKRHPF 320

Qy        236 LAGVLWDHLSEKRVEPGFVPN 256
               : : |: |  : : | | |:
Db        321 FSTIDWNKLYRRELSPPFKPS 341


RESULT 14
A53300
ribosomal protein S6 kinase (EC 2.7.-.-) II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: A53300
R;Grove, J.R.; Price, D.J.; Banerjee, P.; Balasubramanyam, A.; Ahmad, M.F.; Avruch, J.
Biochemistry 32, 7727-7738, 1993
A;Title: Regulation of an epitope-tagged recombinant Rsk-1 S6 kinase by phorbol ester an
A;Reference number: A53300; MUID:93349850; PMID:7688567
A;Accession: A53300
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-735 <RES>
A;Cross-references: UNIPROT:Q63531; UNIPARC:UPI000012DB2D; GB:M99169; NID:g206771; PIDN:
C;Genetics:
A;Gene: Rsk-1
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;60-321/Domain: protein kinase homology <KIN1>
F;68-76/Region: protein kinase ATP-binding motif
F;416-675/Domain: protein kinase homology <KIN2>
F;424-432/Region: protein kinase ATP-binding motif #status atypical

  Query Match             22.0%;  Score 427;  DB 2;  Length 735;
  Best Local Similarity   36.5%;  Pred. No. 1.2e-13;
  Matches   95;  Conservative   50;  Mismatches  101;  Indels   14;  Gaps    5;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| : |     || ||    | :|| :: | |:| | |:|| |  :::::| | |||
Db         90 LYAMKVLKKATLKVRDRVRTKM-ERDILADVNHPFVVKLHYAFQTEGKLYLILDFLRGGD 148

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |   | : | |:|: |: |: |:|| ||:|    ||:||:||:|||||| ||  |||| :
Db        149 LFTRLSKEVMFTEEDVKFYLAELALGLDHLHSLGIIYRDLKPENILLDEEGHIKLTDFGL 208

Qy        121 ATIIKDGE-RATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              :    | | :| :  ||  |||||: :       |::   |||| ||: :|:| |  |:
Db        209 SKEAIDHEKKAYSFCGTVEYMAPEVVNR-----QGHTHSADWWSYGVLMFEMLTGSLPFQ 263

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSS----LQDVQAAPA 235
                 :|:       |::   | |  :||| |   |  :|| |     ::::
Db        264 GKDRKETMTLILKAKLGMPQFLST---EAQSLLRALFKRNPANRLGSGPDGAEEIKRHIF 320

Qy        236 LAGVLWDHLSEKRVEPGFVP 255
               : : |: |  : ::| | |
Db        321 YSTIDWNKLYRREIKPPFKP 340


RESULT 15
S48986
probable protein kinase SCH9 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YHR205w
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 05-Oct-2004
C;Accession: S48986; S30022; A28429
R;Macri, C.
submitted to the EMBL Data Library, February 1994
A;Description: The sequence of S. cerevisiae cosmid 9177.
A;Reference number: S46671
A;Accession: S48986
A;Molecule type: DNA
A;Residues: 1-823 <MAC>
A;Cross-references: UNIPROT:P11792; UNIPARC:UPI0000135644; EMBL:U00029; NID:g551322; PIDN
R;di Blasi, F.; Carra, E.; de Vendittis, E.; Masturzo, P.; Burderi, E.; Lambrinoudaki, I.
Yeast 9, 21-32, 1993
A;Title: The SCH9 protein kinase mRNA contains a long 5' leader with a small open reading
A;Reference number: S30021; MUID:93182531; PMID:8442384
A;Accession: S30022
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 'M',1-823 <DIB>
A;Cross-references: UNIPARC:UPI000016834E; EMBL:X57629; NID:g5277; PIDN:CAA40853.1; PID:g
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1991
R;Toda, T.; Cameron, S.; Sass, P.; Wigler, M.
Genes Dev. 2, 517-527, 1988
A;Title: SCH9, a gene of Saccharomyces cerevisiae that encodes a protein distinct from, h
A;Reference number: A28429; MUID:88255839; PMID:3290050
A;Accession: A28429
A;Molecule type: DNA
A;Residues: 'M',1-364,'S',366-749,'K',751-823 <TOD>
A;Cross-references: UNIPARC:UPI0000168E13; EMBL:X12560; NID:g4425; PIDN:CAA31073.1; PID:g
C;Genetics:
A;Gene: SGD:SCH9
A;Cross-references: SGD:S0001248; MIPS:YHR205w
A;Map position: 8R
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;409-670/Domain: protein kinase homology <KIN>
F;417-425/Region: protein kinase ATP-binding motif

  Query Match             21.9%;  Score 425.5;  DB 2;  Length 823;
  Best Local Similarity   34.8%;  Pred. No. 1.6e-13;
```

Matches 92; Conservative 64; Mismatches 91; Indels 17; Gaps 7;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEIL---QEIEHVFLVNLWYSFQDEEDMFMVVDLLL 57
              :|||| ::|:  ::::|: :   |  ||          |:| | :|||   |:::| | :
Db        436 IYAMKVLSKKVIVKKNEIAHTIGERNILVTTASKSSPFIVGLKFSFQTPTDLYLVTDYMS 495

Qy         58 GGDLRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTD 117
              ||:| :|||:  :|||| : || |: |||::|    |::||:||:|||||  |:  | |
Db        496 GGELFWHLQKEGRFSEDRAKFYIAELVLALEHLHDNDIVYRDLKPENILLDANGNIALCD 555

Qy        118 FNIATI-IKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWR 176
              | ::   :||  |     ||  |:|||:    :   |||:  ||:||:||: :|:  ||
Db        556 FGLSKADLKD--RTNTFCGTTEYLAPEL----LLDETGYTKMVDFWSLGVLIFEMCCGWS 609

Qy        177 PYDIHSSNAVESLVQLFSTVSVQYV-PTWSKEMVALLRKLLTVNPEHRLSSLQD---VQA 232
              |:   ::   : : |  :   |::     |:|  : :: ||  ||:||| :: |   ::|
Db        610 PFFAENN---QKMYQKIAFGKVKFPRDVLSQEGRSFVKGLLNRNPKHRLGAIDDGRELRA 666

Qy        233 APALAGVLWDHLSEKRVEPGFVPN 256
              |  | : |: | :|:: | | |:
Db        667 HPFFADIDWEALKQKKIPPPFKPH 690
```

Search completed: May 9, 2006, 10:49:13
Job time : 42 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:45:08 ; Search time 111 Seconds
(without alignments)
2345.405 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 1942
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1942	100.0	369	2	Q5T0Q5_HUMAN	Q5t0q5 homo sapien
2	1942	100.0	486	2	Q86UX6_HUMAN	Q86ux6 homo sapien
3	1937	99.7	369	2	Q86UE1_HUMAN	Q86ue1 homo sapien
4	1873.5	96.5	368	2	Q9BGT4_MACFA	Q9bgt4 macaca fasc
5	1786.5	92.0	488	2	Q8QZV4_MOUSE	Q8qzv4 mus musculu
6	1786.5	92.0	488	2	Q9JJG4_MOUSE	Q9jjg4 mus musculu
7	1576	81.2	381	2	Q5T0Q4_HUMAN	Q5t0q4 homo sapien
8	1453.5	74.8	441	2	Q4RN62_TETNG	Q4rn62 tetraodon n
9	1273.5	65.6	414	2	Q8IY14_HUMAN	Q8iy14 homo sapien
10	1265.5	65.2	414	2	Q9NY57_HUMAN	Q9ny57 homo sapien
11	1260.5	64.9	414	2	Q7TMD3_MOUSE	Q7tmd3 mus musculu
12	1260.5	64.9	414	2	Q9JJX8_MOUSE	Q9jjx8 mus musculu
13	1259.5	64.9	414	2	Q8C4E0_MOUSE	Q8c4e0 mus musculu
14	1249.5	64.3	364	2	Q6UXH3_HUMAN	Q6uxh3 homo sapien
15	1157	59.6	398	2	Q8BGW6_MOUSE	Q8bgw6 m mus muscu
16	1146.5	59.0	396	2	Q5RAZ7_PONPY	Q5raz7 pongo pygma
17	1125.5	58.0	337	2	Q5RF90_PONPY	Q5rf90 pongo pygma
18	1125	57.9	396	2	Q6GQ72_XENLA	Q6gq72 xenopus lae
19	1030	53.0	368	2	Q7TPQ4_MOUSE	Q7tpq4 mus musculu
20	810	41.7	367	2	Q4RZ50_TETNG	Q4rz50 tetraodon n
21	754	38.8	379	2	Q21483_CAEEL	Q21483 caenorhabdi
22	753	38.8	380	2	Q60Y37_CAEBR	Q60y37 caenorhabdi
23	654.5	33.7	509	2	Q4P7E0_USTMA	Q4p7e0 ustilago ma
24	647.5	33.3	700	2	Q9VN23_DROME	Q9vn23 drosophila
25	636.5	32.8	484	2	Q5KM47_CRYNE	Q5km47 cryptococcu
26	636.5	32.8	484	2	Q55XU6_CRYNE	Q55xu6 cryptococcu
27	603.5	31.1	214	2	Q69YP0_HUMAN	Q69yp0 homo sapien
28	588	30.3	567	2	Q52DZ2_MAGGR	Q52dz2 magnaporthe
29	581	29.9	367	2	Q96WJ8_BLUGR	Q96wj8 blumeria gr
30	577.5	29.7	522	2	Q4I2C7_GIBZE	Q4i2c7 gibberella
31	541	27.9	567	2	Q4WMP1_ASPFU	Q4wmp1 aspergillus
32	489	25.2	166	2	Q8WU08_HUMAN	Q8wu08 homo sapien
33	477	24.6	444	1	KRAC_DICDI	P54644 dictyosteli
34	477	24.6	444	2	Q55EY2_DICDI	Q55ey2 dictyosteli
35	474.5	24.4	210	2	Q5TV49_ANOGA	Q5tv49 anopheles g
36	469	24.2	708	2	Q7QDB4_ANOGA	Q7qdb4 anopheles g
37	467	24.0	456	2	Q8MYF1_DICDI	Q8myf1 dictyosteli
38	466	24.0	442	2	Q810Z3_MOUSE	Q810z3 mus musculu
39	466	24.0	708	2	Q8CHM5_MOUSE	Q8chm5 mus musculu
40	466	24.0	733	1	KS6A2_MOUSE	Q9wut3 m ribosomal
41	465	23.9	758	2	Q9BE29_MACFA	Q9be29 macaca fasc
42	462	23.8	733	2	Q7TPD5_MOUSE	Q7tpd5 mus musculu
43	458	23.6	733	1	KS6A2_HUMAN	Q15349 homo sapien
44	458	23.6	758	2	Q5TI68_HUMAN	Q5ti68 homo sapien
45	458	23.6	806	2	Q59GJ3_HUMAN	Q59gj3 homo sapien

ALIGNMENTS

RESULT 1
Q5T0Q5_HUMAN
ID Q5T0Q5_HUMAN PRELIMINARY; PRT; 369 AA.
AC Q5T0Q5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Protein kinase (PKE).
GN Name=RP11-140A10.1; ORFNames=RP11-140A10.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL512622; CAI12187.1; -; Genomic_DNA.
DR Ensembl; ENSG00000165752; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 369 AA; 42425 MW; 83C54C4AF7D792E5 CRC64;

Query Match 100.0%; Score 1942; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.8e-120;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
                |||||||||
Db        361 PICPSAGSG 369


RESULT 2
Q86UX6_HUMAN
ID   Q86UX6_HUMAN PRELIMINARY;      PRT;   486 AA.
AC   Q86UX6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   PKE protein kinase.
GN   Name=STK32C; Synonyms=RP11-140A10.1; ORFNames=RP11-140A10.1-002;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ma A.-H., Nelson D.A., Xia L., Ravi L., Chen H.-C., Robinson D.R.,
RA   Kung H.-J.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Brown J.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AY098866; AAM21719.1; -; mRNA.
DR   EMBL; AL512622; CAI12181.1; -; Genomic_DNA.
DR   EMBL; AL590105; CAI13011.1; -; Genomic_DNA.
DR   EMBL; AL590105; CAI12181.1; JOINED; Genomic_DNA.
DR   EMBL; AL512622; CAI13011.1; JOINED; Genomic_DNA.
DR   HSSP; P31751; 1MRV.
DR   Ensembl; ENSG00000165752; Homo sapiens.
DR   HGNC; HGNC:21332; STK32C.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   486 AA;  54994 MW;  38FEFBB3863B21F3 CRC64;

  Query Match            100.0%;  Score 1942;  DB 2;  Length 486;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-120;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 477

Qy        361 PICPSAGSG 369
                |||||||||
Db        478 PICPSAGSG 486


RESULT 3
Q86UE1_HUMAN
ID   Q86UE1_HUMAN PRELIMINARY;      PRT;   369 AA.
AC   Q86UE1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   STK32C protein.
GN   Name=STK32C;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RG   NIH MGC Project;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC045760; AAH45760.1; -; mRNA.
```

```
DR   HSSP; P31751; 1MRV.
DR   Ensembl; ENSG00000165752; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   369 AA;  42395 MW;  E152C66BB2D786B4 CRC64;

  Query Match             99.7%;  Score 1937;  DB 2;  Length 369;
  Best Local Similarity   99.7%;  Pred. No. 8.2e-120;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLAVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369


RESULT 4
Q9BGT4_MACFA
ID   Q9BGT4_MACFA PRELIMINARY;      PRT;   368 AA.
AC   Q9BGT4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Frontal lobe left;
RA   Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB056389; BAB33045.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   368 AA;  42218 MW;  5D7269B32DABCC14 CRC64;

  Query Match             96.5%;  Score 1873.5;  DB 2;  Length 368;
  Best Local Similarity   97.0%;  Pred. No. 1.3e-115;
  Matches  358;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELGILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLCGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSLGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSLGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              |||||||||||||||||||||||||:|||||||||||||| ||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSREMVALLRKLLTVNPEHRFSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              | ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WGHLSEKRVEPDFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              |||||||||||||||||||||||||||||| ||||||| |||||||||| |:|||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPSEPLPAPEPRDAAEPVEDE-EQSALPMCG 359

Qy        361 PICPSAGSG 369
              |||||||||
Db        360 PICPSAGSG 368


RESULT 5
Q8QZV4_MOUSE
ID   Q8QZV4_MOUSE PRELIMINARY;      PRT;   488 AA.
AC   Q8QZV4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Serine/threonine kinase 32C (Mus musculus adult male corpora
DE   quadrigemina cDNA, RIKEN full-length enriched library,
DE   clone:B230385A21 product:hypothetical serine/threonine protein kinase,
DE   full insert sequence).
GN   Name=Stk32c;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
```

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC026457; AAH26457.1; -; mRNA.
DR EMBL; AK046439; BAC32730.1; -; mRNA.
DR HSSP; P31751; 1MRV.
DR MGI; MGI:2385336; Stk32c.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 55263 MW; 2B6A927BE6B78EF2 CRC64;

Query Match 92.0%; Score 1786.5; DB 2; Length 488;
Best Local Similarity 92.4%; Pred. No. 9.9e-110;
Matches 341; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 119 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 178

```
Qy          61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
               ||||||||||||||||||||||||||||||| |||||||||||||||:||||||||||
Db         179 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 238

Qy         121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         239 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 298

Qy         181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
               |||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db         299 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 358

Qy         241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
               || ||||:|||||||||||||||||||||||||||||||||||||||||:|||||||
Db         359 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 418

Qy         301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVED-EAERSALPMC 359
               |||||||||||||||||||||||||:|  || | ||: |  :   | ||| :|||||
Db         419 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSDMTDSTADSEAEPTALPMC 478

Qy         360 GPICPSAGS 368
               | ||||:||
Db         479 GSICPSSGS 487


RESULT 6
Q9JJG4_MOUSE
ID   Q9JJG4_MOUSE PRELIMINARY;      PRT;   488 AA.
AC   Q9JJG4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus brain cDNA, clone MNCb-1563, similar to AJ250840
DE   serine/threonine protein kinase (Mus musculus).
GN   Name=Stk32c; Synonyms=Pkek;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL;
RA   Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA   Hashimoto K.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AB041542; BAA95027.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   Ensembl; ENSMUSG00000015981; Mus musculus.
DR   MGI; MGI:2385336; Stk32c.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   488 AA;  55277 MW;  310483FF69E24E39 CRC64;

  Query Match             92.0%;  Score 1786.5;  DB 2;  Length 488;
  Best Local Similarity   92.4%;  Pred. No. 9.9e-110;
  Matches  341;  Conservative   10;  Mismatches   17;  Indels    1;  Gaps    1;

Qy           1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         119 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 178

Qy          61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
               ||||||||||||||||||||||||||||||| |||||||||||||||:||||||||||
Db         179 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 238

Qy         121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         239 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 298

Qy         181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
               |||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db         299 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 358

Qy         241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
               || ||||:|||||||||||||||||||||||||||||||||||||||||:|||||||
Db         359 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 418

Qy         301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVED-EAERSALPMC 359
               |||||||||||||||||||||||||:|  || | ||: |  :   | ||| :|||||
Db         419 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSDMTDSTADSEAEPTALPMC 478

Qy         360 GPICPSAGS 368
               | ||||:||
Db         479 GSICPSSGS 487


RESULT 7
Q5T0Q4_HUMAN
ID   Q5T0Q4_HUMAN PRELIMINARY;      PRT;   381 AA.
AC   Q5T0Q4;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Protein kinase (PKE).
GN   Name=RP11-140A10.1; ORFNames=RP11-140A10.1-004;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AL512622; CAI12188.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   381 AA;  43102 MW;  6564FFB4CDF5E333 CRC64;

  Query Match             81.2%;  Score 1576;  DB 2;  Length 381;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-96;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 116

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 176

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 236

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 296

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 356


RESULT 8
Q4RN62_TETNG
ID   Q4RN62_TETNG PRELIMINARY;      PRT;   441 AA.
AC   Q4RN62;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome undetermined SCAF15016, whole genome shotgun sequence.
GN   ORFNames=GSTENG00031718001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01015016; CAG10170.1; -; Genomic_DNA.
SQ   SEQUENCE   441 AA;  50816 MW;  71C81AC5A8E49E63 CRC64;

  Query Match             74.8%;  Score 1453.5;  DB 2;  Length 441;
  Best Local Similarity   72.9%;  Pred. No. 8.5e-88;
  Matches  275;  Conservative   27;  Mismatches   20;  Indels   55;  Gaps    2;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 125

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIH---------------------- 97
                |||||||:|||||| ||||:||| |||||| |||||
Db        126 LRYHLQQSVQFSEDAVRLYLCEMTLALDYLQSQHIIHSLYSEAEVKPKPRLITAGPLLCN 185

Qy         98 ------------------------------RDVKPDNILLDERGHAHLTDFNIATIIKD 126
                                           ||||||||||||||||||||||||||||
Db        186 LLPPYDISFSYKEQMAPGGKLAALNGPACSVTDVKPDNILLDERGHAHLTDFNIATIIKD 245

Qy        127 GERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAV 186
                |||||||||||||||||| |||||||||:|||||||:||  :|:|||||||||||:||:|
Db        246 GERATALAGTKPYMAPEIFQSFVNGGTGYAFEVDWWSLGVTVFEVLRGWRPYDIHASNSV 305

Qy        187 ESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSE 246
                |||:|||||:|||| | | |::|:|||||||||||| ||| |:| :| || : || : |
Db        306 ESLIQLFSTISVQYSPAWPKDLVSLLRKLLTVNPEHRFSSLSDMQTSPYLADINWDAVYE 365

Qy        247 KRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQ 306
                |::| ||||||||||||||||||||||||||||||||||||:|||||:| |||||||||
Db        366 KKMEAGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNRSRDNSKD-SQSENDYLQ 424

Qy        307 DCLDAIQQDFVIFNREK 323
                :||| :||:|:|||||:
Db        425 ECLDVVQQEFMIFNRER 441


RESULT 9
Q8IY14_HUMAN
ID   Q8IY14_HUMAN PRELIMINARY;      PRT;   414 AA.
AC   Q8IY14;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Serine/threonine kinase 32B.
GN   Name=STK32B;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC038238; AAH38238.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   Ensembl; ENSG00000152953; Homo sapiens.
DR   HGNC; HGNC:14217; STK32B.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
```

```
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   414 AA;  47784 MW;  F0E5EE695FA8242F CRC64;

  Query Match             65.6%;  Score 1273.5;  DB 2;  Length 414;
  Best Local Similarity   69.8%;  Pred. No. 6.1e-76;
  Matches  229;  Conservative   50;  Mismatches   48;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||:|||||||||||||||:|:| :|| ||||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||| |:| ||:|||||:||||:||:  ||||||:||||||||| || |:|||||
Db        108 LRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||::|  |||:::||||||||||:|  :::|| |||: |||||:|: ||||||||||:|
Db        168 ATVVKGAERASSMAGTKPYMAPEVFQVYMDGGPGYSYPVDWWSLGITAYELLRGWRPYEI 227

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||   :: :: :|    | |  || | |||||||||| :|| |:||| |:|: | || :
Db        228 HSVTPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMN 287

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || : :| : ||||||||||:|||||||||||||:||||||||||||:||| ::||
Db        288 WDAVFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL 347

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
               | :|| ||: ::::|:|||||||:| |
Db        348 -NGHLQHCLETVREEFIIFNREKLRRQQ 374


RESULT 10
Q9NY57_HUMAN
ID   Q9NY57_HUMAN PRELIMINARY;      PRT;   414 AA.
AC   Q9NY57;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Serine/threonine protein kinase.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole brain cDNA;
RX   MEDLINE=20164328; PubMed=10700184; DOI=10.1038/73508;
RA   Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA   King L., Francomano C., Freisinger P., Spranger S., Marino B.,
RA   Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,
RA   Goodship J.;
RT   "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers
RT   acrodental dysostosis.";
RL   Nat. Genet. 24:283-286(2000).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AJ250839; CAB76471.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   414 AA;  47883 MW;  8FCD58A67EF09B0E CRC64;

  Query Match             65.2%;  Score 1265.5;  DB 2;  Length 414;
  Best Local Similarity   69.5%;  Pred. No. 2e-75;
  Matches  228;  Conservative   50;  Mismatches   49;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||:|||||||||||||:|:| :|| ||||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||| |:| ||:|||||:||||:||:  ||||||:||||||||| || |:|||||
Db        108 LRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||::|  |||:::||||||||||:|  ::: | |||: |||||:|: ||||||||||:|
Db        168 ATVVKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEI 227

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||   :: :: :|    | |  || | |||||||||| :|| |:||| |:|: | || :
Db        228 HSVTPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMN 287

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || : :| : ||||||||||:|||||||||||||:||||||||||||:||| ::||
Db        288 WDAVFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL 347

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
               | :|| ||: ::::|:|||||||:| |
Db        348 -NGHLQHCLETVREEFIIFNREKLRRQQ 374


RESULT 11
Q7TMD3_MOUSE
ID   Q7TMD3_MOUSE PRELIMINARY;      PRT;   414 AA.
AC   Q7TMD3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Serine/threonine kinase 32B.
GN   Name=Stk32b;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain, and Mouse;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
```

```
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
RA   Strausberg R.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC052404; AAH52404.1; -; mRNA.
DR   EMBL; BC058412; AAH58412.1; -; mRNA.
DR   EMBL; BC056396; AAH56396.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   Ensembl; ENSMUSG00000015981; Mus musculus.
DR   MGI; MGI:1927552; Stk32b.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   414 AA;  47916 MW;  3C394415790594F3 CRC64;

  Query Match             64.9%;  Score 1260.5;  DB 2;  Length 414;
  Best Local Similarity   68.9%;  Pred. No. 4.4e-75;
  Matches  226;  Conservative   55;  Mismatches   46;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||||:|:|||||||||||||:|:| :|| |||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||  |:| ||:|||||:||||:||:  ||||||:|||||||||  || |:|||||
Db        108 LRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||::|  |:|:::|||||||||:|  :|:|| |||: |||||:|| ||||||||||:|
Db        168 ATVLKGSEKASSMAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVTAYELLRGWRPYEI 227

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||:  :: :: :|    | |  || : ||:||:|||| :|| |||||:|:|:   || :
Db        228 HSATPIDEILNMFKVERVHYSSTWCEGMVSLLKKLLTKDPESRLSSLRDIQSMTYLADMN 287

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || : || : |||||||||:|||||||||||||:||||||||||::|||:::||
Db        288 WDAVFEKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKHRSRDSTKDSCPL 347

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
               | :|| ||: ::::|:|||||||:| |
Db        348 -NGHLQQCLETVRKEFIIFNREKLRRQQ 374


RESULT 12
Q9JJX8_MOUSE
ID   Q9JJX8_MOUSE PRELIMINARY;      PRT;   414 AA.
AC   Q9JJX8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Serine/threonine protein kinase.
GN   Name=Stk32b; Synonyms=Stk32;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain cDNA;
RX   MEDLINE=20164328; PubMed=10700184; DOI=10.1038/73508;
RA   Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA   King L., Francomano C., Freisinger P., Spranger S., Marino B.,
RA   Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,
RA   Goodship J.;
RT   "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers
RT   acrodental dysostosis.";
RL   Nat. Genet. 24:283-286(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AJ250840; CAB76566.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   Ensembl; ENSMUSG00000015981; Mus musculus.
DR   MGI; MGI:1927552; Stk32b.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   414 AA;  47917 MW;  BE394415790B9A13 CRC64;

  Query Match             64.9%;  Score 1260.5;  DB 2;  Length 414;
  Best Local Similarity   68.9%;  Pred. No. 4.4e-75;
  Matches  226;  Conservative   55;  Mismatches   46;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||:|:|||||||||||:|:| :|| |||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||  |:| ||:|||||:||||:||:  ||||||:|||||||||  || |:|||||
Db        108 LRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||::|  |:|:::|||||||||:|  :|:|| |||: |||||:|| ||||||||||:|
Db        168 ATVLKGSEKASSMAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVTAYELLRGWRPYEI 227

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||:  :: :: :|    | |  || : ||:||:|||| :|| |||||:|:|:   || :
Db        228 HSATPIDEILNMFKVERVHYSSTWCEGMVSLLKKLLTKDPESRLSSLRDIQSMTYLADMN 287

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || : || : |||||||||:|||||||||||||:||||||||||::|||:::||
Db        288 WDAVFEKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKHRSRDSTKDSCPL 347

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
               | :|| ||: ::::|:|||||||:| |
Db        348 -NGHLQQCLETVRKEFIIFNREKLRRQQ 374
```

```
RESULT 13
Q8C4E0_MOUSE
ID   Q8C4E0_MOUSE PRELIMINARY;      PRT;   414 AA.
AC   Q8C4E0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
DE   library, clone:C230053G02 product:serine threonine kinase 32, full
DE   insert sequence.
GN   Name=Stk32b; Synonyms=Stk32;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AK082468; BAC38500.1; -; mRNA.
DR   HSSP; P31751; 1MRV.
DR   MGI; MGI:1927552; Stk32b.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   414 AA;  47884 MW;  9C394364BE19E945 CRC64;

  Query Match             64.9%;  Score 1259.5;  DB 2;  Length 414;
  Best Local Similarity   68.9%;  Pred. No. 5.1e-75;
  Matches  226;  Conservative   55;  Mismatches   46;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||:|:|||||||||||||:|:| :|| ||||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||| |:| ||:|||||:||||:||:  ||||||:||||||||| || |:||||
Db        108 LRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||::|  |:|:::||||||||||:|  :|:|| ||||: |||||:|| ||||||||||:|
Db        168 ATVLKGSEKASSVAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVTAYELLRGWRPYEI 227

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||:  :: :: :|     | |  || : ||:||:|||| :|| |||||:|:|:   || :
Db        228 HSATPIDEILNMFKVERVHYSSTWCEGMVSLLKKLLTKDPESRLSSLRDIQSMTYLADMN 287

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || : || : |||||||||:|||||||||||||:||||||||||::|||:::||
Db        288 WDAVFEKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKHRSRDSTKDSCPL 347

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
                | :|| ||: ::::|:|||||||:| |
Db        348 -NGHLQQCLETVRKEFIIFNREKLRRQQ 374


RESULT 14
Q6UXH3_HUMAN
ID   Q6UXH3_HUMAN PRELIMINARY;      PRT;   364 AA.
```

```
AC   Q6UXH3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   HSA250839.
GN   ORFNames=UNQ3003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358353; AAQ88719.1; -; mRNA.
DR   HSSP; P05132; 1APM.
DR   Ensembl; ENSG00000152953; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ   SEQUENCE   364 AA;  42195 MW;  FE52D0CB54C7A27C CRC64;

  Query Match           64.3%;  Score 1249.5;  DB 2;  Length 364;
  Best Local Similarity   69.2%;  Pred. No. 2e-74;
  Matches  225;  Conservative   50;  Mismatches   49;  Indels    1;  Gaps    1;

Qy          4 MKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 63
              |||||||:|||||||||||||||:|:| :|| |||||||||||||||||||||||||||||
Db          1 MKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 60

Qy         64 HLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATI 123
              |||||| |:| ||:|||||:||||:||:  ||||||:||||||||| || |:|||||||:
Db         61 HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV 120

Qy        124 IKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSS 183
              :|  |||:::|||||||||:|  ::: | |||: |||||:|: ||||||||||||:|||
Db        121 VKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEIHSV 180

Qy        184 NAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDH 243
                :: :: :|    | |  || | |||||||||| :|| |:||| |:|: | || : ||
Db        181 TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA 240

Qy        244 LSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSEND 303
              : :| : ||||||||||:|||||||||||||:|||||||||||||:||| ::||    |
Db        241 VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL-NG 299

Qy        304 YLQDCLDAIQQDFVIFNREKLKRSQ 328
              :|| ||: ::::|:|||||||:| |
Db        300 HLQHCLETVREEFIIFNREKLRRQQ 324
```

```
RESULT 15
Q8BGW6_MOUSE
ID   Q8BGW6_MOUSE PRELIMINARY;      PRT;   398 AA.
AC   Q8BGW6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DE   enriched library, clone:9630050F05 product:SIMILAR TO SERINE THREONINE
DE   KINASE 32 homolog (Mus musculus 7 days neonate cerebellum cDNA, RIKEN
DE   full-length enriched library, clone:A730009C22 product:SIMILAR TO
DE   SERINE THREONINE KINASE 32 homolog) (Mus musculus adult retina cDNA,
DE   RIKEN full-length enriched library, clone:A930015B13 product:SIMILAR
DE   TO SERINE THREONINE KINASE 32 homolog).
GN   Name=Stk32a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
```

```
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AK036266; BAC29366.1; -; mRNA.
DR   EMBL; AK042599; BAC31302.1; -; mRNA.
DR   EMBL; AK044474; BAC31941.1; -; mRNA.
DR   HSSP; P31751; 1GZK.
DR   Ensembl; ENSMUSG00000039954; Mus musculus.
DR   MGI; MGI:2442403; Stk32a.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.

SQ   SEQUENCE   398 AA;  46509 MW;  689BCA5B25CF18BB CRC64;

  Query Match             59.6%;  Score 1157;  DB 2;  Length 398;
  Best Local Similarity   63.0%;  Pred. No. 2.8e-68;
  Matches  220;  Conservative   51;  Mismatches   74;  Indels    4;  Gaps    2;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||:|:||:||||||:||:|:| :|| ||||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||| | ||||:|:|||:|:|||||: | |||||:||||||||| || |:|||||
Db        108 LRYHLQQNVHFQEDTVKLFICELAMALDYLQSQRIIHRDMKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              | ::    | | :||||||||||:| |     ||||| |||||:|| ||||||| ||| |
Db        168 AAMLPKETRITTVAGTKPYMAPEMFTS--RKETGYSFAVDWWSLGVTAYELLRGRRPYHI 225

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              || : : :| :| | | | |   ||:|||:||:|||  ||: | | | |:|  | :: :
Db        226 RSSTSSKEIVNMFETAIVTYPSAWSQEMVSLLKKLLEPNPDQRFSHLTDIQNFPYMSDMN 285

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || : :||: |||:| ||||:||||||||||||:|||||||||| :      ||||:
Db        286 WDAVLQKRLIPGFIPTKGRLNCDPTFELEEMILESKPLHKKKKRLAKREKEMKKSDSSQT 345

Qy        301 ENDYLQDCLDAIQQDFVIFNRE-KLKRSQDLPREPLPAPESRDAAEPVED 349
                 ||: |||:|::|:|||||:|   :  :  |   ::::  |  ||
Db        346 --CLLQEHLDAVQKEFIIFNREKVKSDFNQRQANLALEQTKNNTEEEED 392


Search completed: May  9, 2006, 10:47:45
Job time : 114 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:42:46 ; Search time 185 Seconds
(without alignments)
876.383 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 1942
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1942	100.0	369	5	ABB84299	Abb84299 Human ser
2	1942	100.0	369	7	ADJ70605	Adj70605 Human hea
3	1942	100.0	486	8	ADJ96618	Adj96618 Human YAN
4	1942	100.0	486	8	ADK71861	Adk71861 Human kin
5	1939	99.8	425	4	AAM40592	Aam40592 Human pol
6	1933	99.5	419	4	AAB65599	Aab65599 Novel pro
7	1933	99.5	419	8	ADI29204	Adi29204 Human MAR
8	1927.5	99.3	488	6	ABO14992	Abo14992 Human NOV
9	1924	99.1	419	4	AAM38806	Aam38806 Human pol
10	1873.5	96.5	368	5	ABB84301	Abb84301 Macaque s
11	1856.5	95.6	713	5	ABB06090	Abb06090 Human NS
12	1845	95.0	364	5	AAO17708	Aao17708 Human ser
13	1827.5	94.1	485	5	AAE24141	Aae24141 Human kin
14	1786.5	92.0	399	5	ABB84300	Abb84300 Murine se
15	1786.5	92.0	488	5	AAO17709	Aao17709 Murine se
16	1710	88.1	384	6	ABU62279	Abu62279 Mouse ser
17	1710	88.1	384	8	ADL09166	Adl09166 Mouse ser
18	1710	88.1	384	9	ADZ58502	Adz58502 Mouse ser
19	1693	87.2	444	6	AAE37974	Aae37974 Human kin
20	1576	81.2	375	4	AAE04371	Aae04371 Human kin
21	1576	81.2	442	7	ADG74653	Adg74653 Human kin
22	1340	69.0	429	4	AAB71961	Aab71961 Human TGF
23	1265.5	65.2	403	6	ABU62278	Abu62278 Human ser
24	1265.5	65.2	403	8	ADL09165	Adl09165 Human ser
25	1265.5	65.2	403	9	ADZ58501	Adz58501 Human ser
26	1265.5	65.2	414	4	AAB65600	Aab65600 Novel pro
27	1265.5	65.2	414	5	ABP43807	Abp43807 Serine/th
28	1265.5	65.2	414	5	AAO17710	Aao17710 Human ser
29	1265.5	65.2	414	6	ABR58617	Abr58617 Human can
30	1265.5	65.2	414	7	ADE38375	Ade38375 Human pro
31	1265.5	65.2	414	8	ADI29205	Adi29205 Human MAR
32	1265.5	65.2	414	8	ADQ17598	Adq17598 Human sof
33	1260.5	64.9	403	9	ADZ58505	Adz58505 Mouse ser
34	1250	64.4	404	6	ABU62277	Abu62277 Mouse ser
35	1250	64.4	404	8	ADL09164	Adl09164 Mouse ser
36	1250	64.4	404	9	ADZ58500	Adz58500 Mouse ser
37	1249.5	64.3	364	4	AAU29309	Aau29309 Human PRO
38	1249.5	64.3	364	6	ABU58685	Abu58685 Human PRO
39	1249.5	64.3	364	6	ABU88233	Abu88233 Novel hum
40	1249.5	64.3	364	6	ABU84548	Abu84548 Human sec
41	1249.5	64.3	364	6	ABR66422	Abr66422 Human sec
42	1249.5	64.3	364	6	ABR65812	Abr65812 Human sec
43	1249.5	64.3	364	6	ABU99752	Abu99752 Human sec
44	1249.5	64.3	364	6	ABU82991	Abu82991 Human PRO
45	1249.5	64.3	364	6	ABU90112	Abu90112 Novel hum

ALIGNMENTS

RESULT 1
ABB84299
ID ABB84299 standard; protein; 369 AA.
XX
AC ABB84299;
XX
DT 12-NOV-2002 (first entry)
XX
DE Human serine/threonine protein kinase subfamily-related protein.
XX
KW Serine/threonine protein kinase subfamily; chromosome 10; human; enzyme;
KW cytostatic; gene therapy; drug screening; tissue typing; prostate; lung;
KW pharmacogenomic; brain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 42. .45
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 75. .77
FT /note= "protein kinase C phosphorylation site"
FT Region 95. .107
FT /note= "serine/threonine protein kinase active signature
FT motif"
FT Modified-site 152. .157
FT /note= "N-myristoylation site"
FT Region 185. .205
FT /note= "helix region"
FT Modified-site 226. .229
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 245. .247
FT /note= "protein kinase C phosphorylation site"
FT Modified-site 288. .291
FT /note= "N-glycosylation site"
FT Modified-site 298. .301
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 300. .303
FT /note= "casein kinase II phosphorylation site"
XX
PN WO200259288-A2.
XX
PD 01-AUG-2002.
XX
PF 15-JAN-2002; 2002WO-US000930.
XX
PR 23-JAN-2001; 2001US-0263162P.
PR 29-MAR-2001; 2001US-00819607.

```
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Beasley EM,  Ye J,  Yan C,  Ketchum KA,  Di Francesco V;
XX
DR   WPI; 2002-599781/64.
DR   N-PSDB; ABQ76181, ABQ76182.
XX
PT   New peptides related to serine/threonine protein kinase subfamily, useful
PT   for treating disorders associated with abnormal expression of kinase in
PT   prostate, lungs and brain, in drug screening assays and pharmacogenomic
PT   analysis.
XX
PS   Claim 1; Fig 2A; 86pp; English.
XX
CC   This invention describes a novel serine/threonine protein kinase
CC   subfamily-associated protein isolated from human chromosome 10 which has
CC   cytostatic activity and can be used for gene therapy. The products of the
CC   invention are useful in substantial and specific assays related to
CC   functional information of the peptide sequences, to raise antibodies or
CC   to elicit immune response, as reagents in assays to determine the levels
CC   of protein in biological fluids, and as markers for tissues where the
CC   corresponding protein is expressed. The peptides and antibodies are
CC   useful in drug screening assays, tissue typing and pharmacogenomic
CC   analysis. They are also useful in treating disorders associated with the
CC   absence of, inappropriate, or unwanted expression of kinase protein in
CC   prostate, lungs or brain. The nucleic acid molecules are useful for
CC   probes, primers and chemical intermediates in biological assays, for
CC   constructing recombinant vectors, expressing antigenic portions of the
CC   protein. The peptide and nucleic acid sequences are useful as models for
CC   the development of human therapeutic targets, aid in the identification
CC   of therapeutic proteins and serve as targets for the development of human
CC   therapeutic agents that modulate kinase activity in cells and tissues
CC   that express the kinase. The host cells are useful in producing a kinase
CC   protein or peptide, and non-human transgenic animals. This sequence
CC   represents the human serine/threonine protein kinase subfamily-associated
CC   protein described in the disclosure of the invention
XX
SQ   Sequence 369 AA;

  Query Match             100.0%;  Score 1942;  DB 5;  Length 369;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-178;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369
```

```
RESULT 2
ADJ70605
ID   ADJ70605 standard; protein; 369 AA.
XX
AC   ADJ70605;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID2411.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2003087768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS,  Fahy ED,  Zhang B,  Gibson BW,  Taylor SW,  Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 2411; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 369 AA;

  Query Match             100.0%;  Score 1942;  DB 7;  Length 369;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-178;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369
```

RESULT 3
ADJ96618
ID ADJ96618 standard; protein; 486 AA.
XX
AC ADJ96618;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human YANK3 protein SeqID 75.
XX
KW kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
KW PTK; STK; gene therapy; cancer; immune-related disease;
KW cardiovascular disease; brain; neuronal associated disease; metabolic;
KW inflammatory disorder; cytostatic; neuroprotective; immunomodulator;
KW antiinflammatory; enzyme; YANK3.
XX
OS Homo sapiens.
OS 28.
XX
PN WO2004006838-A2.
XX
PD 22-JAN-2004.
XX
PF 15-JUL-2003; 2003WO-US021730.
XX
PR 15-JUL-2002; 2002US-0395632P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Whyte D, Manning G, Caenepeel S;
XX
DR WPI; 2004-122753/12.
DR N-PSDB; ADJ96552.
XX
PT New nucleic acid molecule encoding a kinase polypeptide, useful for
PT preparing a composition for treating diseases or disorders, e.g., cancer,
PT or neurological, immunological or inflammatory disorders.
XX
PS Claim 1; SEQ ID NO 75; 366pp; English.
XX
CC This invention relates to a novel isolated, enriched or purified nucleic
CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
CC as well as protein kinase-like enzymes. The present invention describes
CC screening methods to identify agonists, antagonists and antibodies that
CC can be used to modulate the activity or function of the mammalian kinase
CC enzymes. As such, these compositions can be used for gene therapy
CC purposes to treat diseases or disorders including cancer, immune-related
CC diseases, cardiovascular disease, brain or neuronal associated disease,
CC metabolic and inflammatory disorders. Accordingly, they exhibit
CC cytostatic, neuroprotective, immunomodulator and antiinflammatory
CC activities. This polypeptide sequence is a human kinase protein sequence
CC of the invention.
XX
SQ Sequence 486 AA;

```
  Query Match             100.0%;  Score 1942;  DB 8;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-178;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 477

Qy        361 PICPSAGSG 369
              |||||||||
Db        478 PICPSAGSG 486
```

RESULT 4
ADK71861
ID ADK71861 standard; protein; 486 AA.
XX
AC ADK71861;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human kinase and phosphatase KPP-38 protein.
XX
KW human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
KW hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV;
KW antiallergic; antiasthmatic; immunosuppressive; antithyroid;
KW dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal;
KW neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological;
KW antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;
KW antipsoriatic; haemostatic; cytostatic; antilipaemic; antiparasitic;
KW antihelmintic; antibacterial; virucide; protozoacide; fungicide;
KW cardiovascular disease; immune system; neurological; growth; development;
KW cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; enzyme;
KW single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO2004018641-A2.
XX
PD 04-MAR-2004.
XX
PF 25-AUG-2003; 2003WO-US026635.
XX
PR 26-AUG-2002; 2002US-0406172P.
PR 25-SEP-2002; 2002US-0413910P.
PR 27-SEP-2002; 2002US-0414296P.

PR 11-OCT-2002; 2002US-0417821P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
PI Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
PI Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
PI Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
PI Murage J;
XX
DR WPI; 2004-226830/21.
DR N-PSDB; ADK71920.
XX
PT New human kinases and phosphatases, useful for diagnosing, treating or
PT preventing atherosclerosis, hypertension, AIDS, allergy, multiple
PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
PT or hepatitis.
XX
PS Claim 1; SEQ ID NO 38; 347pp; English.
XX
CC The invention relates to a novel isolated polypeptide which is a human
CC kinase and phosphatase (KPP). The polypeptide of the invention
CC demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
CC vasotropic, antiinflammatory, antianginal, anti-HIV, antiallergic,
CC antiasthmatic, immunosuppressive, antithyroid, dermatological,
CC antidiabetic, nephrotropic, antigout, gastrointestinal, neuroprotective,
CC osteopathic, antiarthritic, uropathic, ophthalmological, antirheumatic,
CC antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic,
CC haemostatic, cytostatic, antilipaemic, antiparasitic, antihelmintic,
CC antibacterial, virucide, protozoacide and fungicide activities. The
CC kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and
CC antagonists may be useful for diagnosing, treating or preventing
CC disorders such as cardiovascular diseases, immune system disorders,
CC neurological disorders, disorders affecting growth and development, cell
CC proliferative disorders and viral, bacterial, fungal, parasitic,
CC protozoan or helminthic infections. Furthermore, the molecules of the
CC invention may be useful for creating transgenic animals to model human
CC disease and during gene therapy. The current sequence is that of a human
CC KPP protein of the invention.
XX
SQ Sequence 486 AA;

Query Match 100.0%; Score 1942; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 5.1e-178;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 477

Qy        361 PICPSAGSG 369
              |||||||||
Db        478 PICPSAGSG 486
```

RESULT 5
AAM40592
ID AAM40592 standard; protein; 425 AA.
XX
AC AAM40592;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5523.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI59748.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 2; SEQ ID NO 5523; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 425 AA;

Query Match 99.8%; Score 1939; DB 4; Length 425;
Best Local Similarity 99.7%; Pred. No. 8.2e-178;
Matches 368; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 116

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 176

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 236

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 296

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 356

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 416

Qy        361 PICPSAGSG 369
              |||||||||
Db        417 PICPSAGSG 425
```

RESULT 6
AAB65599
ID AAB65599 standard; protein; 419 AA.
XX
AC AAB65599;
XX
DT 27-MAR-2001 (first entry)
XX
DE Novel protein kinase, SEQ ID NO: 124.
XX
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS Homo sapiens.
XX
PN WO200073469-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014842.
XX
PR 28-MAY-1999; 99US-0136503P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
DR WPI; 2001-032161/04.
DR N-PSDB; AAF44624.
XX
PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
XX
PS Claim 10; Fig 1; 310pp; English.
XX
CC The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX
SQ Sequence 419 AA;

Query Match 99.5%; Score 1933; DB 4; Length 419;
Best Local Similarity 99.7%; Pred. No. 3.1e-177;
Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFXSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419
```

RESULT 7
ADI29204
ID ADI29204 standard; protein; 419 AA.
XX
AC ADI29204;
XX
DT 22-APR-2004 (first entry)
XX
DE Human MARK3-associated protein #2.
XX
KW Human; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disorde;
KW hyperproliferative disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003232771-A1.
XX
PD 18-DEC-2003.
XX
PF 17-JUN-2002; 2002US-00174319.
XX
PR 17-JUN-2002; 2002US-00174319.

XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Freier SM, Dobie KW;
XX
DR WPI; 2004-052188/05.
DR N-PSDB; ADI29322.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
PT expression of MARK3 or for treating cancer or Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 124; 233pp; English.
XX
CC The invention relates to a compound comprising a sequence comprising 8-80
CC base pairs (bp) targeted to a nucleic acid encoding MARK3
CC (MAP/microtubule affinity-regulating kinase 3), that specifically
CC hybridises with the nucleic acid encoding MARK3 and inhibits expression
CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
CC composition comprising the compound and a carrier or diluent, inhibiting
CC the expression of MARK3 in cells or tissues, treating an animal having or
CC suspected of having a disease or condition associated with MARK3 and
CC screening for an antisense compound. The antisense oligonucleotide is
CC useful for preparing a composition for treating hyperproliferative
CC disorder, particularly cancer and neurodegenerative diseases e.g.
CC Alzheimer's disease. The present sequence is a MARK3 associated protein
CC included in the figures but not mentioned anywhere else in the
CC specification.
XX
SQ Sequence 419 AA;

Query Match 99.5%; Score 1933; DB 8; Length 419;
Best Local Similarity 99.7%; Pred. No. 3.1e-177;
Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFXSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419
```

RESULT 8
ABO14992
ID ABO14992 standard; protein; 488 AA.
XX
AC ABO14992;
XX
DT 26-AUG-2003 (first entry)
XX
DE Human NOV5 protein.
XX
KW Human; NOVX; inflammatory disorder; demyelination disease; stroke;
KW renal disorder; infection; cardiomyopathy; atherosclerosis; acne;
KW hypertension; pancreatitis; Von Hippel-Lindau; endometriosis; fertility;
KW scleroderma; cirrhosis; inflammatory bowel disease; Crohn's disease;
KW haemophilia; autoimmune disease; allergy; AIDS;
KW graft versus host disease; Alzheimer's disease; arthritis; pain;
KW Parkinson's disease; Huntington's disease; obesity; diabetes;
KW hair growth; hair loss; asthma; schizophrenia; glomerulonephritis;
KW lupus erythematosus; psoriasis; antidiabetic; anorectic; metabolic;
KW nootropic; neuroprotective; cytostatic; antibacterial; virucide;
KW protozoacide; antiarteriosclerotic; hypotensive; cerebroprotective;
KW antiinflammatory; gynaecological; antiinfertility; dermatological;
KW hepatotropic; haemostatic; immunosuppressive; antiallergic;
KW antiarthritic; anticonvulsant; antiseborrhoeic; antiasthmatic;
KW neuroleptic; anti-HIV; analgesic; nephrotropic; antipsoriatic.
XX
OS Homo sapiens.
XX
PN WO200298917-A2.
XX
PD 12-DEC-2002.
XX
PF 12-FEB-2002; 2002WO-US022049.
XX
PR 12-FEB-2001; 2001US-0268221P.
PR 13-FEB-2001; 2001US-0268496P.
PR 14-FEB-2001; 2001US-0268646P.
PR 14-FEB-2001; 2001US-0268665P.
PR 15-FEB-2001; 2001US-0269136P.
PR 16-FEB-2001; 2001US-0269310P.
PR 16-FEB-2001; 2001US-0269530P.
PR 15-MAR-2001; 2001US-0276405P.
PR 16-MAR-2001; 2001US-0276399P.
PR 16-MAR-2001; 2001US-0276703P.
PR 23-MAR-2001; 2001US-0278199P.
PR 28-MAR-2001; 2001US-0279274P.
PR 30-MAR-2001; 2001US-0280238P.
PR 02-APR-2001; 2001US-0280899P.
PR 08-AUG-2001; 2001US-0310797P.
PR 14-AUG-2001; 2001US-0312284P.
PR 14-SEP-2001; 2001US-0322294P.
PR 14-SEP-2001; 2001US-0322295P.
PR 18-OCT-2001; 2001US-0330293P.
PR 31-OCT-2001; 2001US-0335104P.
PR 31-OCT-2001; 2001US-0335109P.
PR 21-NOV-2001; 2001US-0332127P.
PR 28-NOV-2001; 2001US-0331772P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Guo X, Fernandes E, Li L, Kekuda R, Liu Y, Leite M, Spytek KA;
PI Ji W, Casman SJ, Boldog FL, Patturajan M, Vernet CAM, Ballinger RA;
PI Malyankar UM, Tchernev VT, Blalock AD, Gusev VY, Rastelli L;
PI Mezes PD, Ellerman K, Heyes M, Herrmann JL, Shimkets RA, Ioime N;
PI Pena CEA, Shenoy SG, Taupier RJ, Gerlach V, Gorman L;
XX
DR WPI; 2003-148650/14.
DR N-PSDB; ACD20380.
XX
PT Novel NOVX polypeptide useful for identifying an agent that binds to the
PT polypeptide, and for treating cardiomyopathy, atherosclerosis,
PT hypertension, infertility, scleroderma, cirrhosis, and inflammatory bowel
PT disease.
XX
PS Claim 1; Page 41; 566pp; English.
XX
CC The present invention relates to the isolation of novel human
CC polypeptides referred to as NOVX (NOV1-NOV37), variants of these
CC proteins, and the polynucleotide sequences encoding them. The NOVX
CC proteins of the invention share homology to varies types of protein
CC families such as zinc finger-like proteins, enzymes, receptors, and
CC lipoproteins. The sequences of the invention may be useful in the

```
CC   manufacture of a medicament for treating a syndrome associated with a
CC   human disease. For example they can be used to treat inflammatory
CC   disorders, demyelination disease, renal disorders, infections,
CC   cardiomyopathy, atherosclerosis, hypertension, stroke, pancreatitis, Von
CC   Hippel-Lindau, endometriosis, fertility, scleroderma, cirrhosis,
CC   inflammatory bowel disease, Crohn's disease, haemophilia, autoimmune
CC   diseases, allergies, graft versus host disease, Alzheimer's disease,
CC   arthritis, Parkinson's disease, Huntington's disease, obesity, diabetes,
CC   acne, hair growth/loss, asthma, schizophrenia, AIDS, pain,
CC   glomerulonephritis, lupus erythematosus, and psoriasis. ABO14984-ABO15039
CC   represent the NOVX polypeptides of the invention. Note: SEQ ID Nos 113-
CC   460 are known sequences used for homology purposes
XX
SQ   Sequence 488 AA;

  Query Match             99.3%;  Score 1927.5;  DB 6;  Length 488;
  Best Local Similarity   99.5%;  Pred. No. 1.3e-176;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 178

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 238

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 298

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRK-LLTVNPEHRLSSLQDVQAAPALAGV 239
              |||||||||||||||||||||||||||||| |||| ||||||||||||||||||||||||
Db        299 HSSNAVESLVQLFSTVSVQYVPTWSKEMVGLLRKVLLTVNPEHRLSSLQDVQAAPALAGV 358

Qy        240 LWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQ 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 LWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQ 418

Qy        300 SENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMC 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 SENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMC 478

Qy        360 GPICPSAGSG 369
              ||||||||||
Db        479 GPICPSAGSG 488


RESULT 9
AAM38806
ID   AAM38806 standard; protein; 419 AA.
XX
AC   AAM38806;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 1951.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI57962.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Example 3; SEQ ID NO 1951; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 419 AA;

  Query Match             99.1%;  Score 1924;  DB 4;  Length 419;
  Best Local Similarity   99.5%;  Pred. No. 2.3e-176;
  Matches  367;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNVVTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419
```

RESULT 10
ABB84301
ID ABB84301 standard; protein; 368 AA.
XX
AC ABB84301;
XX
DT 12-NOV-2002 (first entry)
XX
DE Macaque serine/threonine protein kinase subfamily-related protein.
XX
KW Serine/threonine protein kinase subfamily; chromosome 10; enzyme;
KW cytostatic; gene therapy; drug screening; tissue typing; prostate; lung;
KW pharmacogenomic; brain; macaque.
XX
OS Macaca fascicularis.
XX
PN WO200259288-A2.
XX
PD 01-AUG-2002.
XX
PF 15-JAN-2002; 2002WO-US000930.
XX
PR 23-JAN-2001; 2001US-0263162P.
PR 29-MAR-2001; 2001US-00819607.
XX
PA (PEKE) PE CORP NY.
XX
PI Beasley EM, Ye J, Yan C, Ketchum KA, Di Francesco V;
XX
DR WPI; 2002-599781/64.
XX
PT New peptides related to serine/threonine protein kinase subfamily, useful
PT for treating disorders associated with abnormal expression of kinase in
PT prostate, lungs and brain, in drug screening assays and pharmacogenomic
PT analysis.
XX
PS Disclosure; Fig 2B-C; 86pp; English.
XX
CC This invention describes a novel serine/threonine protein kinase
CC subfamily-associated protein isolated from human chromosome 10 which has
CC cytostatic activity and can be used for gene therapy. The products of the
CC invention are useful in substantial and specific assays related to
CC functional information of the peptide sequences, to raise antibodies or
CC to elicit immune response, as reagents in assays to determine the levels
CC of protein in biological fluids, and as markers for tissues where the
CC corresponding protein is expressed. The peptides and antibodies are
CC useful in drug screening assays, tissue typing and pharmacogenomic
CC analysis. They are also useful in treating disorders associated with the
CC absence of, inappropriate, or unwanted expression of kinase protein in
CC prostate, lungs or brain. The nucleic acid molecules are useful for
CC probes, primers and chemical intermediates in biological assays, for
CC constructing recombinant vectors, expressing antigenic portions of the
CC protein. The peptide and nucleic acid sequences are useful as models for
CC the development of human therapeutic targets, aid in the identification
CC of therapeutic proteins and serve as targets for the development of human
CC therapeutic agents that modulate kinase activity in cells and tissues
CC that express the kinase. The host cells are useful in producing a kinase
CC protein or peptide, and non-human transgenic animals. This sequence
CC represents a macaque (macaca fascicularis) serine/threonine protein
CC kinase subfamily-associated protein described in the disclosure of the
CC invention
XX
SQ Sequence 368 AA;

Query Match 96.5%; Score 1873.5; DB 5; Length 368;
Best Local Similarity 97.0%; Pred. No. 1.4e-171;
Matches 358; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELGILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLCGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSLGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              |||||||||||||||||||||||:|||||||||||||| ||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSREMVALLRKLLTVNPEHRFSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              | |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WGHLSEKRVEPDFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              |||||||||||||||||||||||||||||| ||||||| |||||||||| |:||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPSEPLPAPEPRDAAEPVEDE-EQSALPMCG 359

Qy        361 PICPSAGSG 369
              |||||||||
Db        360 PICPSAGSG 368
```

RESULT 11
ABB06090
ID ABB06090 standard; protein; 713 AA.
XX
AC ABB06090;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human NS protein sequence SEQ ID NO:182.
XX
KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
KW anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic;
KW gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW infertility; cardiovascular disease; coagulation disease; hypertension;
KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW gastric ulcer; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200206315-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-IL000653.
XX
PR 18-JUL-2000; 2000IL-00137345.
PR 15-DEC-2000; 2000IL-00140354.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Mintz L, Freilich S, Bernstein J;
XX
DR WPI; 2002-155037/20.
DR N-PSDB; ABL39744.
XX
PT One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
XX

```
PS   Claim 6; Page 207-209; 290pp; English.
XX
CC   ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC   encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC   (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC   antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC   vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC   anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
CC   anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant,
CC   immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer,
CC   antidepressant, gastrointestinal, aeuroleptic, cerebroprotective,
CC   nootropic and contraceptive activities. The NS can be used in vaccines,
CC   gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC   antibodies from the present invention can be used for treating and
CC   diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC   diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC   cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC   glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC   disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC   disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC   depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC   Alzheimer's disease and as a contraceptive
XX
SQ   Sequence 713 AA;

  Query Match             95.6%;  Score 1856.5;  DB 5;  Length 713;
  Best Local Similarity   92.5%;  Pred. No. 1.6e-169;
  Matches  358;  Conservative    0;  Mismatches    6;  Indels   23;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||||||||||||||||| | ||| ||||||||||||||||||||||||||||
Db        160 MYAMKYMNKQQCIERDEVRNVFREXEXLQEXEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 219

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 279

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 339

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 399

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 459

Qy        301 ------------------------ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPA 337
                                       |||||||||||||||||||||||||| ||||||||
Db        460 APRSXSKPSTQRQGSWALASSGWENDYLQDCLDAIQQDFVIFNREKLKRSQALPREPLPA 519

Qy        338 PESRDAAEPVEDEAERSALPMCGPICP 364
              |||||||||||||| |||||||||| |
Db        520 PESRDAAEPVEDEAVRSALPMCGPIVP 546


RESULT 12
AAO17708
ID   AAO17708 standard; protein; 364 AA.
XX
AC   AAO17708;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Human serine-threonine protein kinase.
XX
KW   Human; serine-threonine protein kinase; cancer; diabetes; obesity;
KW   central nervous system disorder; inflammation; gene therapy; COPD;
KW   neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;
KW   antidiabetic; antiallergic; antiasthmatic; antidepressant; anorectic;
KW   antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;
KW   enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200233056-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-EP011892.
XX
PR   16-OCT-2000; 2000US-0240097P.
PR   30-JUL-2001; 2001US-0308096P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Koehler RH;
XX
DR   WPI; 2002-435534/46.
DR   N-PSDB; AAL46714.
XX
PT   New human serine-threonine protein kinase and encoding polynucleotides,
PT   useful for diagnosing, treating and preventing central nervous system
PT   disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
XX
PS   Claim 25; Fig 2; 135pp; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   human serine-threonine protein kinase. The sequences can be used in the
CC   diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma
CC   or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or
CC   traumatic brain injury), diabetes, eating disorders (e.g. obesity,
CC   anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and
CC   chronic obstructive pulmonary disease (COPD). The present sequence is the
CC   protein of the invention
XX
SQ   Sequence 364 AA;

  Query Match             95.0%;  Score 1845;  DB 5;  Length 364;
  Best Local Similarity   99.7%;  Pred. No. 7.7e-169;
  Matches  351;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 72

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 132

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 192

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 252

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 312

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAE 352
              |||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        313 ENDYLQDCLDAIQQDFVIFNREKMKRSQDLPREPLPAPESRDAAEPVEDEAE 364


RESULT 13
AAE24141
ID   AAE24141 standard; protein; 485 AA.
XX
AC   AAE24141;
XX
DT   23-SEP-2002  (first entry)
```

```
XX
DE   Human kinase (PKIN)-12 protein.
XX
KW   Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;
KW   acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;
KW   asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;
KW   development; hepatitis; cardiovascular; hypertension; drug screening;
KW   myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;
KW   fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;
KW   hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hIV;
KW   neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;
KW   hyperlipidaemia; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .24
FT                   /label= Signal_peptide
FT   Protein         25. .485
FT                   /note= "Human mature kinase (PKIN)-12"
FT   Domain          65. .372
FT                   /note= "Protein kinase domain"
FT   Domain          93. .372
FT                   /note= "Protein kinase domain"
FT   Domain          93. .345
FT                   /note= "Eukaryotic protein kinase domain"
FT   Domain          95. .342
FT                   /note= "Protein kinase domain"
XX
PN   WO200233099-A2.
XX
PD   25-APR-2002.
XX
PF   20-OCT-2001; 2001WO-US047728.
XX
PR   20-OCT-2000; 2000US-0242410P.
PR   27-OCT-2000; 2000US-0244068P.
PR   03-NOV-2000; 2000US-0245708P.
PR   09-NOV-2000; 2000US-0247672P.
PR   16-NOV-2000; 2000US-0249565P.
PR   22-NOV-2000; 2000US-0252730P.
PR   01-DEC-2000; 2000US-0250807P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Gururajan R,  Baughn MR,  Walia NK,  Elliott VS,  Xu Y,  Arvizu C;
PI   Yao MG,  Ramkumar J,  Ding L,  Tang YT,  Hafalia AJA,  Nguyen DB;
PI   Gandhi AR,  Lu Y,  Yue H,  Burford N,  Bandman O,  Tribouley CM,  Lal PG;
PI   Recipon SA,  Lu DAM,  Borowsky ML,  Thornton M,  Swarnaker A;
PI   Thangavelu K,  Khan FA,  Ison CH;
XX
DR   WPI; 2002-454603/48.
DR   N-PSDB; AAD38855.
XX
PT   New human kinase polypeptide, for diagnosing, preventing and treating
PT   cancer, immune system disorders, growth and development disorders,
PT   cardiovascular disorders and lipid disorders.
XX
PS   Claim 1; Page 160-161; 210pp; English.
XX
CC   The invention relates human kinases (PKIN) and their corresponding
CC   nucleic acid sequences. PKIN and its DNA are useful for diagnosing,
CC   treating and preventing cancer, an immune system disorder (e.g., acquired
CC   immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,
CC   atherosclerosis, multiple sclerosis, psoriasis), disorders affecting
CC   growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),
CC   cardiovascular disorder (e.g., hypertension, myocardial infarction,
CC   Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,
CC   Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,
CC   hyperlipidaemia, obesity), and for assessing the effects of exogenous
CC   compounds. Anti-PKIN antibody is useful in a diagnostic test for a
CC   condition or a disease associated with the expression of PKIN in a
CC   biological sample. A composition comprising PKIN or an agonist or
CC   antagonist of PKIN is useful for treating a disease or condition
CC   associated with decreased or increased expression of functional PKIN.
CC   PKIN is useful in a number of drug screening techniques and to analyse
CC   the proteome of a tissue or cell type. PKIN DNA is useful for creating
CC   knockin humanised animals or transgenic animals to model human diseases,
CC   and in somatic or germline gene therapy. The present sequence is human
CC   PKIN protein
XX
SQ   Sequence 485 AA;

  Query Match             94.1%;  Score 1827.5;  DB 5;  Length 485;
  Best Local Similarity   95.4%;  Pred. No. 5.7e-167;
  Matches  352;  Conservative    1;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||  |       :        |||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPA-LSPGMLRSLWRTRRTLRLPMCG 476

Qy        361 PICPSAGSG 369
              |||||||||
Db        477 PICPSAGSG 485


RESULT 14
ABB84300
ID   ABB84300 standard; protein; 399 AA.
XX
AC   ABB84300;
XX
DT   12-NOV-2002  (first entry)
XX
DE   Murine serine/threonine protein kinase subfamily-related protein.
XX
KW   Serine/threonine protein kinase subfamily; chromosome 10; enzyme; murine;
KW   cytostatic; gene therapy; drug screening; tissue typing; prostate; lung;
KW   pharmacogenomic; brain.
XX
OS   Mus musculus.
XX
PN   WO200259288-A2.
XX
PD   01-AUG-2002.
XX
PF   15-JAN-2002; 2002WO-US000930.
XX
PR   23-JAN-2001; 2001US-0263162P.
PR   29-MAR-2001; 2001US-00819607.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Beasley EM,  Ye J,  Yan C,  Ketchum KA,  Di Francesco V;
XX
DR   WPI; 2002-599781/64.
```

```
XX
PT   New peptides related to serine/threonine protein kinase subfamily, useful
PT   for treating disorders associated with abnormal expression of kinase in
PT   prostate, lungs and brain, in drug screening assays and pharmacogenomic
PT   analysis.
XX
PS   Disclosure; Fig 2B; 86pp; English.
XX
CC   This invention describes a novel serine/threonine protein kinase
CC   subfamily-associated protein isolated from human chromosome 10 which has
CC   cytostatic activity and can be used for gene therapy. The products of the
CC   invention are useful in substantial and specific assays related to
CC   functional information of the peptide sequences, to raise antibodies or
CC   to elicit immune response, as reagents in assays to determine the levels
CC   of protein in biological fluids, and as markers for tissues where the
CC   corresponding protein is expressed. The peptides and antibodies are
CC   useful in drug screening assays, tissue typing and pharmacogenomic
CC   analysis. They are also useful in treating disorders associated with the
CC   absence of, inappropriate, or unwanted expression of kinase protein in
CC   prostate, lungs or brain. The nucleic acid molecules are useful for
CC   probes, primers and chemical intermediates in biological assays, for
CC   constructing recombinant vectors, expressing antigenic portions of the
CC   protein. The peptide and nucleic acid sequences are useful as models for
CC   the development of human therapeutic targets, aid in the identification
CC   of therapeutic proteins and serve as targets for the development of human
CC   therapeutic agents that modulate kinase activity in cells and tissues
CC   that express the kinase. The host cells are useful in producing a kinase
CC   protein or peptide, and non-human transgenic animals. This sequence
CC   represents a murine serine/threonine protein kinase subfamily-associated
CC   protein described in the disclosure of the invention
XX
SQ   Sequence 399 AA;

  Query Match             92.0%;  Score 1786.5;  DB 5;  Length 399;
  Best Local Similarity   92.4%;  Pred. No. 3.8e-163;
  Matches  341;  Conservative   10;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 90

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||||||| ||||||||||||||||:|||||||||||
Db         91 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 150

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 210

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              |||||||||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db        211 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 270

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || ||||:|||||||||||||||||||||||||||||||||||||||||:|||||||
Db        271 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 330

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVED-EAERSALPMC 359
              |||||||||||||||||||||||||:|  || | ||: |  :   | ||| :|||||
Db        331 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSDMTDSTADSEAEPTALPMC 390

Qy        360 GPICPSAGS 368
              | ||||:||
Db        391 GSICPSSGS 399


RESULT 15
AAO17709
ID   AAO17709 standard; protein; 488 AA.
XX
AC   AAO17709;
XX
DT   20-AUG-2002  (first entry)

XX
DE   Murine serine-threonine protein kinase.
XX
KW   Human; serine-threonine protein kinase; cancer; diabetes; obesity;
KW   central nervous system disorder; inflammation; gene therapy; COPD;
KW   neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;
KW   antidiabetic; antiallergic; antiasthmatic; antidepressant; anorectic;
KW   antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;
KW   enzyme.
XX
OS   Mus musculus.
XX
PN   WO200233056-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-EP011892.
XX
PR   16-OCT-2000; 2000US-0240097P.
PR   30-JUL-2001; 2001US-0308096P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Koehler RH;
XX
DR   WPI; 2002-435534/46.
XX
PT   New human serine-threonine protein kinase and encoding polynucleotides,
PT   useful for diagnosing, treating and preventing central nervous system
PT   disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
XX
PS   Disclosure; Fig 3; 135pp; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   human serine-threonine protein kinase. The sequences can be used in the
CC   diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma
CC   or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or
CC   traumatic brain injury), diabetes, eating disorders (e.g. obesity,
CC   anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and
CC   chronic obstructive pulmonary disease (COPD). The present sequence is a
CC   murine serine-threonine protein kinase
XX
SQ   Sequence 488 AA;

  Query Match             92.0%;  Score 1786.5;  DB 5;  Length 488;
  Best Local Similarity   92.4%;  Pred. No. 5.1e-163;
  Matches  341;  Conservative   10;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 178

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||||||| ||||||||||||||||:|||||||||||
Db        179 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 238

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 298

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              |||||||||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db        299 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 358

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || ||||:|||||||||||||||||||||||||||||||||||||||||:|||||||
Db        359 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 418

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVED-EAERSALPMC 359
              |||||||||||||||||||||||||:|  || | ||: |  :   | ||| :|||||
Db        419 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSDMTDSTADSEAEPTALPMC 478

Qy        360 GPICPSAGS 368
```

| |||||:||
Db 479 GSICPSSGS 487

Search completed: May 9, 2006, 10:48:29
Job time : 189 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:45:55 ; Search time 27 Seconds
(without alignments)
1129.901 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 1942
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1942	100.0	369	2	US-09-819-607-2	Sequence 2, Appli
2	1942	100.0	419	2	US-09-799-875-14	Sequence 14, Appl
3	1873.5	96.5	368	2	US-09-819-607-5	Sequence 5, Appli
4	1786.5	92.0	399	2	US-09-819-607-4	Sequence 4, Appli
5	1710	88.1	384	2	US-09-801-876B-6	Sequence 6, Appli
6	1710	88.1	384	2	US-10-254-869-6	Sequence 6, Appli
7	1710	88.1	384	2	US-10-667-442-6	Sequence 6, Appli
8	1265.5	65.2	403	2	US-09-801-876B-5	Sequence 5, Appli
9	1265.5	65.2	403	2	US-10-254-869-5	Sequence 5, Appli
10	1265.5	65.2	403	2	US-10-667-442-5	Sequence 5, Appli
11	1250	64.4	404	2	US-09-801-876B-4	Sequence 4, Appli
12	1250	64.4	404	2	US-10-254-869-4	Sequence 4, Appli
13	1250	64.4	404	2	US-10-667-442-4	Sequence 4, Appli
14	1146.5	59.0	396	2	US-09-841-683-11	Sequence 11, Appl
15	1146.5	59.0	396	2	US-10-620-845-11	Sequence 11, Appl
16	1142	58.8	407	2	US-09-841-683-9	Sequence 9, Appli
17	1142	58.8	407	2	US-10-620-845-9	Sequence 9, Appli
18	1137.5	58.6	396	2	US-09-801-876B-2	Sequence 2, Appli
19	1137.5	58.6	396	2	US-10-254-869-2	Sequence 2, Appli
20	1137.5	58.6	396	2	US-10-667-442-2	Sequence 2, Appli
21	1078.5	55.5	316	2	US-09-801-876B-7	Sequence 7, Appli
22	1078.5	55.5	316	2	US-10-254-869-7	Sequence 7, Appli
23	1078.5	55.5	316	2	US-10-667-442-7	Sequence 7, Appli
24	754	38.8	347	2	US-09-801-876B-8	Sequence 8, Appli
25	754	38.8	347	2	US-10-254-869-8	Sequence 8, Appli
26	754	38.8	347	2	US-10-667-442-8	Sequence 8, Appli
27	709	36.5	225	2	US-09-841-683-5	Sequence 5, Appli
28	709	36.5	225	2	US-10-620-845-5	Sequence 5, Appli
29	709	36.5	236	2	US-09-841-683-7	Sequence 7, Appli
30	709	36.5	236	2	US-10-620-845-7	Sequence 7, Appli
31	453	23.3	380	2	US-09-487-558B-402	Sequence 402, App
32	444	22.9	740	2	US-09-538-092-1178	Sequence 1178, Ap
33	444	22.9	740	2	US-09-771-161A-265	Sequence 265, App
34	444	22.9	740	2	US-09-771-161A-266	Sequence 266, App
35	425.5	21.9	824	2	US-09-487-558B-312	Sequence 312, App
36	424	21.8	587	1	US-08-313-274-2	Sequence 2, Appli
37	424	21.8	655	2	US-09-949-016-11676	Sequence 11676, A
38	423	21.8	260	1	US-07-857-224B-7	Sequence 7, Appli
39	419	21.6	398	2	US-09-538-092-501	Sequence 501, App
40	419	21.6	398	2	US-09-487-558B-404	Sequence 404, App
41	417	21.5	397	2	US-09-487-558B-400	Sequence 400, App
42	416	21.4	480	2	US-09-091-058-2	Sequence 2, Appli
43	416	21.4	480	2	US-09-590-740-2	Sequence 2, Appli
44	416	21.4	480	2	US-09-538-092-1053	Sequence 1053, Ap
45	416	21.4	480	2	US-09-526-043-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-819-607-2
; Sequence 2, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
US-09-819-607-2

Query Match 100.0%; Score 1942; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
```

```
Db        361 PICPSAGSG 369


RESULT 2
US-09-799-875-14
; Sequence 14, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
;  APPLICANT:  Meyers, Rachel
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Williamson, Mark
;  TITLE OF INVENTION:  No. 6638721el Human Protein Kinases and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE:  35800/209996
;  CURRENT APPLICATION NUMBER: US/09/799,875
;  CURRENT FILING DATE:  2001-03-06
;  PRIOR APPLICATION NUMBER:  60/182,059
;  PRIOR FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  09/659,287
;  PRIOR FILING DATE:  2000-09-12
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-799-875-14

  Query Match            100.0%;  Score 1942;  DB 2;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-159;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 3
US-09-819-607-5
; Sequence 5, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001078
;  CURRENT APPLICATION NUMBER: US/09/819,607
;  CURRENT FILING DATE:  2001-03-29
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-09-819-607-5

  Query Match            96.5%;  Score 1873.5;  DB 2;  Length 368;
  Best Local Similarity   97.0%;  Pred. No. 2.3e-153;
  Matches  358;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELGILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLCGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSLGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||:|||||||||||||| ||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSREMVALLRKLLTVNPEHRFSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              | |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WGHLSEKRVEPDFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              |||||||||||||||||||||||||||||||| ||||||| |||||||||| |:||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPSEPLPAPEPRDAAEPVEDE-EQSALPMCG 359

Qy        361 PICPSAGSG 369
              |||||||||
Db        360 PICPSAGSG 368


RESULT 4
US-09-819-607-4
; Sequence 4, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001078
;  CURRENT APPLICATION NUMBER: US/09/819,607
;  CURRENT FILING DATE:  2001-03-29
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 399
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-819-607-4

  Query Match            92.0%;  Score 1786.5;  DB 2;  Length 399;
  Best Local Similarity   92.4%;  Pred. No. 8.1e-146;
  Matches  341;  Conservative   10;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 90

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||||| ||||||||||||||||:||||||||||
Db         91 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 150
```

```
Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 210

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db        211 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 270

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || ||||:|||||||||||||||||||||||||||||||||||||||||:|||||||
Db        271 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 330

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVED-EAERSALPMC 359
              ||||||||||||||||||||||||||:|  || | ||: |  :   | ||| :|||||
Db        331 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSDMTDSTADSEAEPTALPMC 390

Qy        360 GPICPSAGS 368
              | ||||:||
Db        391 GSICPSSGS 399


RESULT 5
US-09-801-876B-6
; Sequence 6, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160
;  CURRENT APPLICATION NUMBER: US/09/801,876B
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-09-801-876B-6

  Query Match             88.1%;  Score 1710;  DB 2;  Length 384;
  Best Local Similarity   95.0%;  Pred. No. 3e-139;
  Matches  325;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         43 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 102

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||||||| ||||||||||||||:||||||||||
Db        103 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 162

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 222

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db        223 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 282

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || ||||:|||||||||||||||||||||||||||||||||||||||||:|||||||
Db        283 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 342

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRD 342
              ||||||||||||||||||||||||||:|  || | ||: |
Db        343 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSD 384


RESULT 6
US-10-254-869-6
; Sequence 6, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV
;  CURRENT APPLICATION NUMBER: US/10/254,869
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-254-869-6

  Query Match             88.1%;  Score 1710;  DB 2;  Length 384;
  Best Local Similarity   95.0%;  Pred. No. 3e-139;
  Matches  325;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         43 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 102

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||||||| ||||||||||||||:||||||||||
Db        103 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 162

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 222

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db        223 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 282

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || ||||:|||||||||||||||||||||||||||||||||||||||||:|||||||
Db        283 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 342

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRD 342
              ||||||||||||||||||||||||||:|  || | ||: |
Db        343 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSD 384


RESULT 7
US-10-667-442-6
; Sequence 6, Application US/10667442
; Patent No. 6821765
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV II
;  CURRENT APPLICATION NUMBER: US/10/667,442
;  CURRENT FILING DATE:  2003-09-23
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-667-442-6

  Query Match             88.1%;  Score 1710;  DB 2;  Length 384;
  Best Local Similarity   95.0%;  Pred. No. 3e-139;
  Matches  325;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         43 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 102
```

```
Qy          61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
               |||||||||||||||||||||||||||||| |||||||||||||||:||||||||||
Db         103 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 162

Qy         121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         163 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 222

Qy         181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
               |||||||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db         223 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 282

Qy         241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
               || ||||:||||||||||||||||||||||||||||||||||||||:|||||||
Db         283 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 342

Qy         301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRD 342
               ||||||||||||||||||||||||||:|  || | ||: |
Db         343 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSD 384


RESULT 8
US-09-801-876B-5
; Sequence 5, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160
;  CURRENT APPLICATION NUMBER: US/09/801,876B
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 403
;   TYPE: PRT
;   ORGANISM: Human
US-09-801-876B-5

  Query Match             65.2%;  Score 1265.5;  DB 2;  Length 403;
  Best Local Similarity   69.5%;  Pred. No. 6.7e-101;
  Matches  228;  Conservative   50;  Mismatches   49;  Indels    1;  Gaps    1;

Qy           1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
               ||||||||||:|||||||||||||:|:| :|| ||||||||||||||||||||||||||
Db          48 MYAMKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy          61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
               ||||||||| |:| ||:|||||:||||:||:  ||||||:||||||||| || |:|||||
Db         108 LRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNI 167

Qy         121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
               ||::|  |||:::|||||||||:|  ::: | |||: |||||:|: ||||||||||:|
Db         168 ATVVKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEI 227

Qy         181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
               ||   :: :: :|    | |  || | |||||||||| :|| |:||| |:|: | || :
Db         228 HSVTPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMN 287

Qy         241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
               || : :| : ||||||||||:|||||||||||||:||||||||||||:||| ::||
Db         288 WDAVFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL 347

Qy         301 ENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
                | :|| ||: ::::|:|||||||:| |
Db         348 -NGHLQHCLETVREEFIIFNREKLRRQQ 374


RESULT 9
US-10-254-869-5
```

```
; Sequence 5, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV
;  CURRENT APPLICATION NUMBER: US/10/254,869
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 403
;   TYPE: PRT
;   ORGANISM: Human
US-10-254-869-5

  Query Match             65.2%;  Score 1265.5;  DB 2;  Length 403;
  Best Local Similarity   69.5%;  Pred. No. 6.7e-101;
  Matches  228;  Conservative   50;  Mismatches   49;  Indels    1;  Gaps    1;

Qy           1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
               ||||||||||:|||||||||||||:|:| :|| ||||||||||||||||||||||||||
Db          48 MYAMKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy          61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
               ||||||||| |:| ||:|||||:||||:||:  ||||||:||||||||| || |:|||||
Db         108 LRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNI 167

Qy         121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
               ||::|  |||:::|||||||||:|  ::: | |||: |||||:|: ||||||||||:|
Db         168 ATVVKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEI 227

Qy         181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
               ||   :: :: :|    | |  || | |||||||||| :|| |:||| |:|: | || :
Db         228 HSVTPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMN 287

Qy         241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
               || : :| : ||||||||||:|||||||||||||:||||||||||||:||| ::||
Db         288 WDAVFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL 347

Qy         301 ENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
                | :|| ||: ::::|:|||||||:| |
Db         348 -NGHLQHCLETVREEFIIFNREKLRRQQ 374


RESULT 10
US-10-667-442-5
; Sequence 5, Application US/10667442
; Patent No. 6821765
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV II
;  CURRENT APPLICATION NUMBER: US/10/667,442
;  CURRENT FILING DATE:  2003-09-23
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 403
;   TYPE: PRT
;   ORGANISM: Human
US-10-667-442-5

  Query Match             65.2%;  Score 1265.5;  DB 2;  Length 403;
  Best Local Similarity   69.5%;  Pred. No. 6.7e-101;
  Matches  228;  Conservative   50;  Mismatches   49;  Indels    1;  Gaps    1;

Qy           1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
               ||||||||||:|||||||||||||:|:| :|| ||||||||||||||||||||||||||
```

```
Db         48 MYAMKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||  |:| ||:|||||:||||:||:  ||||||:|||||||| || |:|||||
Db        108 LRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||::|  |||:::|||||||||:|  ::: | |||: |||||:|: ||||||||||:|
Db        168 ATVVKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEI 227

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||   :: :: :|    | |  || | |||||||||| :|| |:||| |:|: | || :
Db        228 HSVTPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMN 287

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || : :| : |||||||||:|||||||||||||:||||||||||:||| ::||
Db        288 WDAVFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL 347

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
               | :|| ||: ::::|:|||||||:| |
Db        348 -NGHLQHCLETVREEFIIFNREKLRRQQ 374


RESULT 11
US-09-801-876B-4
; Sequence 4, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160
;  CURRENT APPLICATION NUMBER: US/09/801,876B
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 404
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-09-801-876B-4

  Query Match             64.4%;  Score 1250;  DB 2;  Length 404;
  Best Local Similarity   68.7%;  Pred. No. 1.5e-99;
  Matches  226;  Conservative   55;  Mismatches   46;  Indels    2;  Gaps    2;

Qy          1 MYAMKYMNKQQCI-ERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGG 59
              ||||||||||:|: |||||||||||:|:| :|| |||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVQERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGG 107

Qy         60 DLRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFN 119
              |||||||||| |:| ||:|||||:||||:||:  ||||||:|||||||| || |:||||
Db        108 DLRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFN 167

Qy        120 IATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              |||::|  |:|:::|||||||||:|  :|:|| ||| |||||:|| ||||||||||:
Db        168 IATVLKGSEKASSMAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVTAYELLRGWRPYE 227

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGV 239
              |||:  :: :: :|    | |  || : ||:||:|||| :|| |||||:|:|:   || :
Db        228 IHSATPIDEILNMFKVERVHYSSTWCEGMVSLLKKLLTKDPESRLSSLRDIQSMTYLADM 287

Qy        240 LWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQ 299
              || : || : |||||||||:|||||||||||||:||||||||||::|||:::||
Db        288 NWDAVFEKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKHRSRDSTKDSCP 347

Qy        300 SENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
               | :|| ||: ::::|:|||||||:| |
Db        348 L-NGHLQQCLETVRKEFIIFNREKLRRQQ 375


RESULT 12
US-10-254-869-4
; Sequence 4, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV
;  CURRENT APPLICATION NUMBER: US/10/254,869
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 404
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-254-869-4

  Query Match             64.4%;  Score 1250;  DB 2;  Length 404;
  Best Local Similarity   68.7%;  Pred. No. 1.5e-99;
  Matches  226;  Conservative   55;  Mismatches   46;  Indels    2;  Gaps    2;

Qy          1 MYAMKYMNKQQCI-ERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGG 59
              ||||||||||:|: |||||||||||:|:| :|| |||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVQERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGG 107

Qy         60 DLRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFN 119
              |||||||||| |:| ||:|||||:||||:||:  ||||||:|||||||| || |:||||
Db        108 DLRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFN 167

Qy        120 IATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              |||::|  |:|:::|||||||||:|  :|:|| ||| |||||:|| ||||||||||:
Db        168 IATVLKGSEKASSMAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVTAYELLRGWRPYE 227

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGV 239
              |||:  :: :: :|    | |  || : ||:||:|||| :|| |||||:|:|:   || :
Db        228 IHSATPIDEILNMFKVERVHYSSTWCEGMVSLLKKLLTKDPESRLSSLRDIQSMTYLADM 287

Qy        240 LWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQ 299
              || : || : |||||||||:|||||||||||||:||||||||||::|||:::||
Db        288 NWDAVFEKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKHRSRDSTKDSCP 347

Qy        300 SENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
               | :|| ||: ::::|:|||||||:| |
Db        348 L-NGHLQQCLETVRKEFIIFNREKLRRQQ 375


RESULT 13
US-10-667-442-4
; Sequence 4, Application US/10667442
; Patent No. 6821765
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001160DIV II
;  CURRENT APPLICATION NUMBER: US/10/667,442
;  CURRENT FILING DATE:  2003-09-23
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 404
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-667-442-4

  Query Match             64.4%;  Score 1250;  DB 2;  Length 404;
  Best Local Similarity   68.7%;  Pred. No. 1.5e-99;
  Matches  226;  Conservative   55;  Mismatches   46;  Indels    2;  Gaps    2;

Qy          1 MYAMKYMNKQQCI-ERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGG 59
```

```
                ||||||||||:|: ||||||||||||:|:| :|| ||||||||||||||||||||||||
Db          48 MYAMKYMNKQKCVQERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGG 107

Qy          60 DLRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFN 119
                |||||||||| |:| ||:|||||:||||:||:  |||||||:||||||||| || |:|||
Db         108 DLRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFN 167

Qy         120 IATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
                |||::|  |:|:::||||||||||:|  :|:|| |||: |||||:|| ||||||||||:
Db         168 IATVLKGSEKASSMAGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVTAYELLRGWRPYE 227

Qy         180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGV 239
                |||:  :: :: :|    | |  || : ||:||:|||| :|| |||||:|:|:   || :
Db         228 IHSATPIDEILNMFKVERVHYSSTWCEGMVSLLKKLLTKDPESRLSSLRDIQSMTYLADM 287

Qy         240 LWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQ 299
                || : || : |||||||||:|||||||||||||:||||||||::|||:::||
Db         288 NWDAVFEKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKHRSRDSTKDSCP 347

Qy         300 SENDYLQDCLDAIQQDFVIFNREKLKRSQ 328
                 | :|| ||: ::::|:|||||||:| |
Db         348 L-NGHLQQCLETVRKEFIIFNREKLRRQQ 375


RESULT 14
US-09-841-683-11
; Sequence 11, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/09/841,683
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-841-683-11

  Query Match             59.0%;  Score 1146.5;  DB 2;  Length 396;
  Best Local Similarity   63.1%;  Pred. No. 1.2e-90;
  Matches  219;  Conservative   47;  Mismatches   72;  Indels    9;  Gaps    3;

Qy           1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
                |||||||||:|:|:|||||:||:|:| :|| ||||||||||||||||||||||||||||
Db          48 MYAMKYMNKQKCVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy          61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
                |||||||| | |:||:|:|||: :|||||: | |||||:|||||||| || |:|||||
Db         108 LRYHLQQNVHFKEETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNI 167

Qy         121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
                | ::    : | :||||||||||:| |    | |||| |||||:|| ||||||| ||| |
Db         168 AAMLPRETQITTMAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGVTAYELLRGRRPYHI 225

Qy         181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
                || : : :|  | |  | |   ||:|||:||:|||  ||: | | | |||  | :  :
Db         226 RSSTSSKEIVHTFETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDIN 285

Qy         241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                || : :||: |||:|||||||:|||||||||||||||:|||||||||| :      ||||:
Db         286 WDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSSQT 345

Qy         301 ENDYLQDCLDAIQQDFVIFNREKL-----KRSQDLPREPLPAPESRD 342
                     ||: ||::|::|:||||||:     ||  :|  |    |:  |
Db         346 --CLLQEHLDSVQKEFIIFNREKVNRDFNKRQPNLALEQTKDPQGED 390


RESULT 15
US-10-620-845-11
; Sequence 11, Application US/10620845
; Patent No. 6908758
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: No. 6908758el Human Kinase Proteins and Polynucleotides Encoding t
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/10/620,845
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-620-845-11

  Query Match             59.0%;  Score 1146.5;  DB 2;  Length 396;
  Best Local Similarity   63.1%;  Pred. No. 1.2e-90;
  Matches  219;  Conservative   47;  Mismatches   72;  Indels    9;  Gaps    3;

Qy           1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
                |||||||||:|:|:|||||:||:|:| :|| ||||||||||||||||||||||||||||
Db          48 MYAMKYMNKQKCVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy          61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
                |||||||| | |:||:|:|||: :|||||: | |||||:|||||||| || |:|||||
Db         108 LRYHLQQNVHFKEETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNI 167

Qy         121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
                | ::    : | :||||||||||:| |    | |||| |||||:|| ||||||| ||| |
Db         168 AAMLPRETQITTMAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGVTAYELLRGRRPYHI 225

Qy         181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
                || : : :|  | |  | |   ||:|||:||:|||  ||: | | | |||  | :  :
Db         226 RSSTSSKEIVHTFETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDIN 285

Qy         241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                || : :||: |||:|||||||:|||||||||||||||:|||||||||| :      ||||:
Db         286 WDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSSQT 345

Qy         301 ENDYLQDCLDAIQQDFVIFNREKL-----KRSQDLPREPLPAPESRD 342
                     ||: ||::|::|:||||||:     ||  :|  |    |:  |
Db         346 --CLLQEHLDSVQKEFIIFNREKVNRDFNKRQPNLALEQTKDPQGED 390


Search completed: May  9, 2006, 10:48:16
Job time : 27 secs
```

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:47:54 ; Search time 78 Seconds
(without alignments)
1976.654 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 1942
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1942	100.0	369	3	US-09-819-607-2	Sequence 2, Appli
2	1942	100.0	369	4	US-10-074-978A-155	Sequence 155, App
3	1942	100.0	369	4	US-10-633-631-2	Sequence 2, Appli
4	1942	100.0	369	4	US-10-408-765A-2411	Sequence 2411, Ap
5	1942	100.0	419	3	US-09-799-875-14	Sequence 14, Appl
6	1942	100.0	419	4	US-10-303-664A-6	Sequence 6, Appli
7	1942	100.0	419	4	US-10-649-156-14	Sequence 14, Appl
8	1942	100.0	486	4	US-10-618-941-75	Sequence 75, Appl
9	1927.5	99.3	488	4	US-10-074-978A-18	Sequence 18, Appl
10	1873.5	96.5	368	3	US-09-819-607-5	Sequence 5, Appli
11	1873.5	96.5	368	4	US-10-074-978A-156	Sequence 156, App
12	1873.5	96.5	368	4	US-10-633-631-5	Sequence 5, Appli
13	1827.5	94.1	485	4	US-10-415-011-12	Sequence 12, Appl
14	1786.5	92.0	399	3	US-09-819-607-4	Sequence 4, Appli
15	1786.5	92.0	399	4	US-10-633-631-4	Sequence 4, Appli
16	1786.5	92.0	488	4	US-10-074-978A-154	Sequence 154, App
17	1710	88.1	384	3	US-09-801-876B-6	Sequence 6, Appli
18	1710	88.1	384	4	US-10-254-869-6	Sequence 6, Appli
19	1710	88.1	384	4	US-10-667-442-6	Sequence 6, Appli
20	1710	88.1	384	5	US-10-962-625-6	Sequence 6, Appli
21	1576	81.2	375	4	US-10-168-582-12	Sequence 12, Appl
22	1265.5	65.2	403	3	US-09-801-876B-5	Sequence 5, Appli
23	1265.5	65.2	403	4	US-10-254-869-5	Sequence 5, Appli
24	1265.5	65.2	403	4	US-10-667-442-5	Sequence 5, Appli
25	1265.5	65.2	403	5	US-10-962-625-5	Sequence 5, Appli
26	1265.5	65.2	414	4	US-10-354-358-36	Sequence 36, Appl
27	1265.5	65.2	414	4	US-10-074-978A-157	Sequence 157, App
28	1265.5	65.2	414	5	US-10-723-860-415	Sequence 415, App
29	1260.5	64.9	414	4	US-10-074-978A-158	Sequence 158, App
30	1250	64.4	404	3	US-09-801-876B-4	Sequence 4, Appli
31	1250	64.4	404	4	US-10-254-869-4	Sequence 4, Appli
32	1250	64.4	404	4	US-10-667-442-4	Sequence 4, Appli
33	1250	64.4	404	5	US-10-962-625-4	Sequence 4, Appli
34	1249.5	64.3	364	4	US-10-052-586-572	Sequence 572, App
35	1249.5	64.3	364	4	US-10-174-590-572	Sequence 572, App
36	1249.5	64.3	364	4	US-10-176-758-572	Sequence 572, App
37	1249.5	64.3	364	4	US-10-175-737-572	Sequence 572, App
38	1249.5	64.3	364	4	US-10-174-581-572	Sequence 572, App
39	1249.5	64.3	364	4	US-10-176-483-572	Sequence 572, App
40	1249.5	64.3	364	4	US-10-176-749-572	Sequence 572, App
41	1249.5	64.3	364	4	US-10-176-914-572	Sequence 572, App
42	1249.5	64.3	364	4	US-10-176-915-572	Sequence 572, App
43	1249.5	64.3	364	4	US-10-173-706-572	Sequence 572, App
44	1249.5	64.3	364	4	US-10-175-738-572	Sequence 572, App
45	1249.5	64.3	364	4	US-10-175-752-572	Sequence 572, App

ALIGNMENTS

RESULT 1
US-09-819-607-2
; Sequence 2, Application US/09819607
; Publication No. US20030022337A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
US-09-819-607-2

Query Match 100.0%; Score 1942; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.4e-143;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
```

```
Db        361 PICPSAGSG 369


RESULT 2
US-10-074-978A-155
; Sequence 155, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-074-978A-155

  Query Match           100.0%;  Score 1942;  DB 4;  Length 369;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-143;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369


RESULT 3
US-10-633-631-2
; Sequence 2, Application US/10633631
; Publication No. US20040067568A1
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001078DIV
;  CURRENT APPLICATION NUMBER: US/10/633,631
;  CURRENT FILING DATE:  2003-08-05
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-633-631-2

  Query Match           100.0%;  Score 1942;  DB 4;  Length 369;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-143;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
```

```
Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369


RESULT 4
US-10-408-765A-2411
; Sequence 2411, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2411
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-2411

  Query Match            100.0%;  Score 1942;  DB 4;  Length 369;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-143;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360

Qy        361 PICPSAGSG 369
              |||||||||
Db        361 PICPSAGSG 369


RESULT 5
US-09-799-875-14
; Sequence 14, Application US/09799875
; Patent No. US20020034780A1
; GENERAL INFORMATION:
;  APPLICANT:  Meyers, Rachel
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Williamson, Mark
;  TITLE OF INVENTION:  No. US20020034780A1el Human Protein Kinases and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE:  35800/209996
;  CURRENT APPLICATION NUMBER: US/09/799,875
;  CURRENT FILING DATE:  2001-03-06
;  PRIOR APPLICATION NUMBER:  60/182,059
;  PRIOR FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  09/659,287
;  PRIOR FILING DATE:  2000-09-12
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-799-875-14

  Query Match            100.0%;  Score 1942;  DB 3;  Length 419;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-143;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 6
US-10-303-664A-6
; Sequence 6, Application US/10303664A
; Publication No. US20030153018A1
; GENERAL INFORMATION:
;  APPLICANT: Hunter, John Joseph
;  APPLICANT:  Williamson, Mark W.
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Rudolph-Owen, Laura A.
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;  TITLE OF INVENTION:  CANCER USING  2192, 2193, 6568, 8895, 9138, 9217, 9609,
;  TITLE OF INVENTION:  9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,
;  TITLE OF INVENTION:  33794, 54476 and 94710
;  FILE REFERENCE: MPI2001-290P3R(M)
;  CURRENT APPLICATION NUMBER: US/10/303,664A
;  CURRENT FILING DATE:  2002-11-25
```

```
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-303-664A-6

  Query Match             100.0%;  Score 1942;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-143;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 7
US-10-649-156-14
; Sequence 14, Application US/10649156
; Publication No. US20040038346A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Williamson, Mark
;  TITLE OF INVENTION: No. US20040038346A1el Human Protein Kinases and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 35800/209996
;  CURRENT APPLICATION NUMBER: US/10/649,156
;  CURRENT FILING DATE:  2003-08-27
;  PRIOR APPLICATION NUMBER: US/09/799,875
;  PRIOR FILING DATE: 2001-03-06
;  PRIOR APPLICATION NUMBER: 60/182,059
;  PRIOR FILING DATE: 2000-02-11
;  PRIOR APPLICATION NUMBER: 09/659,287
;  PRIOR FILING DATE: 2000-09-12
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-649-156-14

  Query Match             100.0%;  Score 1942;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-143;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410

Qy        361 PICPSAGSG 369
              |||||||||
Db        411 PICPSAGSG 419


RESULT 8
US-10-618-941-75
; Sequence 75, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
;  APPLICANT: WHYTE, DAVID
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  CAENEPEEL, SEAN
;  TITLE OF INVENTION: NOVEL KINASES
;  FILE REFERENCE: 034536-0321
;  CURRENT APPLICATION NUMBER: US/10/618,941
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: 60/395,632
;  PRIOR FILING DATE: 2002-07-15
;  NUMBER OF SEQ ID NOS: 143
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
;   LENGTH: 486
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-618-941-75

  Query Match             100.0%;  Score 1942;  DB 4;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 2e-143;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417
```

```
Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 477

Qy        361 PICPSAGSG 369
              |||||||||
Db        478 PICPSAGSG 486


RESULT 9
US-10-074-978A-18
; Sequence 18, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A111e
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 488
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-074-978A-18

  Query Match            99.3%;  Score 1927.5;  DB 4;  Length 488;
  Best Local Similarity  99.5%;  Pred. No. 2.7e-142;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 178

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 238

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 298

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRK-LLTVNPEHRLSSLQDVQAAPALAGV 239
              ||||||||||||||||||||||||||||||||| |||| ||||||||||||||||||||||||
Db        299 HSSNAVESLVQLFSTVSVQYVPTWSKEMVGLLRKVLLTVNPEHRLSSLQDVQAAPALAGV 358

Qy        240 LWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQ 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 LWDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQ 418

Qy        300 SENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMC 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 SENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMC 478

Qy        360 GPICPSAGSG 369
              ||||||||||
Db        479 GPICPSAGSG 488


RESULT 10
US-09-819-607-5
; Sequence 5, Application US/09819607
; Publication No. US20030022337A1
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001078
;  CURRENT APPLICATION NUMBER: US/09/819,607
;  CURRENT FILING DATE:  2001-03-29
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-09-819-607-5

  Query Match            96.5%;  Score 1873.5;  DB 3;  Length 368;
  Best Local Similarity  97.0%;  Pred. No. 3.3e-138;
  Matches  358;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELGILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLCGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSLGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
                |||||||||||||||||||||||:|||||||||||||||| ||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSREMVALLRKLLTVNPEHRFSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                | |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WGHLSEKRVEPDFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
                |||||||||||||||||||||||||||||| ||||||| |||||||||| |:|||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPSEPLPAPEPRDAAEPVEDE-EQSALPMCG 359

Qy        361 PICPSAGSG 369
                |||||||||
Db        360 PICPSAGSG 368


RESULT 11
US-10-074-978A-156
; Sequence 156, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Macaca fuscata
US-10-074-978A-156

  Query Match             96.5%;  Score 1873.5;  DB 4;  Length 368;
  Best Local Similarity   97.0%;  Pred. No. 3.3e-138;
  Matches  358;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELGILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLCGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSLGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              |||||||||||||||||||||||:|||||||||||||||| ||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSREMVALLRKLLTVNPEHRFSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              | |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WGHLSEKRVEPDFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              |||||||||||||||||||||||||||||| ||||||| |||||||||| |:|||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPSEPLPAPEPRDAAEPVEDE-EQSALPMCG 359

Qy        361 PICPSAGSG 369
              |||||||||
Db        360 PICPSAGSG 368


RESULT 12
US-10-633-631-5
; Sequence 5, Application US/10633631
; Publication No. US20040067568A1
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001078DIV
;  CURRENT APPLICATION NUMBER: US/10/633,631
;  CURRENT FILING DATE:  2003-08-05
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-10-633-631-5

  Query Match             96.5%;  Score 1873.5;  DB 4;  Length 368;
  Best Local Similarity   97.0%;  Pred. No. 3.3e-138;
  Matches  358;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;
```

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MYAMKYMNKQQCIERDEVRNVFRELGILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLCGQHIIHRDVKPDNILLDERGHAHLTDFNI 120

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSLGVMAYELLRGWRPYDI 180

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              |||||||||||||||||||||||:||||||||||||||| ||||||||||||||||||||
Db        181 HSSNAVESLVQLFSTVSVQYVPTWSREMVALLRKLLTVNPEHRFSSLQDVQAAPALAGVL 240

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              | |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WGHLSEKRVEPDFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              |||||||||||||||||||||||||||||| ||||||| |||||||||| |:|||||||
Db        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPSEPLPAPEPRDAAEPVEDE-EQSALPMCG 359

Qy        361 PICPSAGSG 369
              |||||||||
Db        360 PICPSAGSG 368
```

RESULT 13
US-10-415-011-12
; Sequence 12, Application US/10415011
; Publication No. US20040053394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: NGUYEN, Danniel B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/47728
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040053394A1 7473788CD1
US-10-415-011-12

Query Match 94.1%; Score 1827.5; DB 4; Length 485;
Best Local Similarity 95.4%; Pred. No. 1.8e-134;
Matches 352; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 297

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 357

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 417

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
              |||||||||||||||||||||||||||||||| |     :     |||||
Db        418 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPA-LSPGMLRSLWRTRRTLRLPMCG 476

Qy        361 PICPSAGSG 369
              |||||||||
Db        477 PICPSAGSG 485
```

RESULT 14
US-09-819-607-4
; Sequence 4, Application US/09819607
; Publication No. US20030022337A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-819-607-4

```
  Query Match             92.0%;  Score 1786.5;  DB 3;  Length 399;
  Best Local Similarity   92.4%;  Pred. No. 2.3e-131;
  Matches  341;  Conservative   10;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 90

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||||||| |||||||||||||||:||||||||||
Db         91 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 150

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 210

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              |||||||||||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db        211 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 270

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || ||||:|||||||||||||||||||||||||||||||||||||||||||:|||||||
Db        271 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 330

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVED-EAERSALPMC 359
              |||||||||||||||||||||||||:|  || | ||: |  :   | ||| :|||||
Db        331 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSDMTDSTADSEAEPTALPMC 390

Qy        360 GPICPSAGS 368
              | ||||:||
Db        391 GSICPSSGS 399


RESULT 15
US-10-633-631-4
; Sequence 4, Application US/10633631
; Publication No. US20040067568A1
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001078DIV
;  CURRENT APPLICATION NUMBER: US/10/633,631
;  CURRENT FILING DATE:  2003-08-05
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 399
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-633-631-4

  Query Match             92.0%;  Score 1786.5;  DB 4;  Length 399;
  Best Local Similarity   92.4%;  Pred. No. 2.3e-131;
  Matches  341;  Conservative   10;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 90

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||||||||||||||||||||||||| |||||||||||||||:||||||||||
Db         91 LRYHLQQNVQFSEDTVRLYICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNI 150

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 210

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
              |||||||||||||||||||||||||||||||||||||||||||||| |||||:| ||:|| ||
Db        211 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVL 270

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || ||||:|||||||||||||||||||||||||||||||||||||||||||:|||||||
Db        271 WDDLSEKKVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQS 330

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVED-EAERSALPMC 359
              |||||||||||||||||||||||||:|  || | ||: |  :   | ||| :|||||
Db        331 ENDYLQDCLDAIQQDFVIFNREKLKRSQELMSEPPPGPETSDMTDSTADSEAEPTALPMC 390

Qy        360 GPICPSAGS 368
              | ||||:||
Db        391 GSICPSSGS 399


Search completed: May  9, 2006, 10:49:40
Job time : 79 secs
```

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 10:48:24 ; Search time 17 Seconds
(without alignments)
1004.651 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 1942
Sequence: 1 MYAMKYMNKQQCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep1:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep1:*
8: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
9: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep1:*
10: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
11: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep1:*
12: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1576	81.2	375	9	US-10-979-095-12	Sequence 12, Appl
2	1249.5	64.3	364	9	US-10-194-487-572	Sequence 572, App
3	1249.5	64.3	364	9	US-10-195-883-572	Sequence 572, App
4	1249.5	64.3	364	9	US-10-195-888-572	Sequence 572, App
5	1249.5	64.3	364	9	US-10-195-889-572	Sequence 572, App
6	1146.5	59.0	396	11	US-11-125-295-11	Sequence 11, Appl
7	1142	58.8	407	11	US-11-125-295-9	Sequence 9, Appli
8	709	36.5	225	11	US-11-125-295-5	Sequence 5, Appli
9	709	36.5	236	11	US-11-125-295-7	Sequence 7, Appli
10	458	23.6	733	8	US-10-505-928-349	Sequence 349, App
11	444	22.9	740	9	US-10-878-556A-129	Sequence 129, App
12	435.5	22.4	502	11	US-11-188-298-19312	Sequence 19312, A
13	435	22.4	385	11	US-11-096-568A-31309	Sequence 31309, A
14	435	22.4	424	11	US-11-096-568A-31308	Sequence 31308, A
15	435	22.4	471	11	US-11-096-568A-31307	Sequence 31307, A
16	433.5	22.3	490	11	US-11-188-298-9166	Sequence 9166, Ap
17	432.5	22.3	480	11	US-11-188-298-1665	Sequence 1665, Ap
18	429.5	22.1	480	11	US-11-132-142-6	Sequence 6, Appli
19	427.5	22.0	518	11	US-11-188-298-11340	Sequence 11340, A
20	426.5	22.0	539	11	US-11-188-298-13310	Sequence 13310, A
21	425.5	21.9	522	11	US-11-188-298-1229	Sequence 1229, Ap
22	423	21.8	480	11	US-11-188-298-17953	Sequence 17953, A
23	422.5	21.8	640	11	US-11-087-099-9638	Sequence 9638, Ap
24	420	21.6	442	11	US-11-188-298-16028	Sequence 16028, A
25	419.5	21.6	472	11	US-11-087-099-10553	Sequence 10553, A
26	419	21.6	398	11	US-11-132-142-7	Sequence 7, Appli
27	418	21.5	555	11	US-11-188-298-3933	Sequence 3933, Ap
28	417.5	21.5	404	11	US-11-087-099-2344	Sequence 2344, Ap
29	417.5	21.5	404	11	US-11-188-298-2276	Sequence 2276, Ap
30	417.5	21.5	424	11	US-11-087-099-5546	Sequence 5546, Ap
31	417.5	21.5	424	11	US-11-188-298-16105	Sequence 16105, A
32	417.5	21.5	425	11	US-11-087-099-1247	Sequence 1247, Ap
33	417.5	21.5	425	11	US-11-188-298-1278	Sequence 1278, Ap
34	417	21.5	555	11	US-11-188-298-21317	Sequence 21317, A
35	416	21.4	480	8	US-10-511-814-6	Sequence 6, Appli
36	416	21.4	480	11	US-11-109-156-18	Sequence 18, Appl
37	414	21.3	411	11	US-11-188-298-13738	Sequence 13738, A
38	414	21.3	556	11	US-11-188-298-13437	Sequence 13437, A
39	413	21.3	360	9	US-10-501-035-298	Sequence 298, App
40	413	21.3	556	11	US-11-188-298-1509	Sequence 1509, Ap
41	411.5	21.2	332	11	US-11-188-298-18718	Sequence 18718, A
42	411.5	21.2	462	11	US-11-132-142-10	Sequence 10, Appl
43	411	21.2	515	11	US-11-132-142-8	Sequence 8, Appli
44	411	21.2	515	11	US-11-188-298-15437	Sequence 15437, A
45	410.5	21.1	353	11	US-11-132-142-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-979-095-12
; Sequence 12, Application US/10979095
; Publication No. US20060068481A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; APPLICANT: KAHN, Farrah A.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0002 PCT
; CURRENT APPLICATION NUMBER: US/10/979,095
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/10/168,582
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 3244919CD1
US-10-979-095-12

Query Match 81.2%; Score 1576; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-114;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 110

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
```

```
Db        111 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180

Db        171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 230

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240

Db        231 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 290

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300

Db        291 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 350
```

RESULT 2
US-10-194-487-572
; Sequence 572, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C312
; CURRENT APPLICATION NUMBER: US/10/194,487
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-487-572

Query Match 64.3%; Score 1249.5; DB 9; Length 364;
Best Local Similarity 69.2%; Pred. No. 2.2e-89;
Matches 225; Conservative 50; Mismatches 49; Indels 1; Gaps 1;

```
Qy          4 MKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 63

Db          1 MKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 60

Qy         64 HLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATI 123

Db         61 HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV 120

Qy        124 IKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSS 183

Db        121 VKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEIHSV 180

Qy        184 NAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDH 243

Db        181 TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA 240

Qy        244 LSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSEND 303

Db        241 VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL-NG 299

Qy        304 YLQDCLDAIQQDFVIFNREKLKRSQ 328

Db        300 HLQHCLETVREEFIIFNREKLRRQQ 324
```

RESULT 3
US-10-195-883-572
; Sequence 572, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C323
; CURRENT APPLICATION NUMBER: US/10/195,883
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-883-572

Query Match 64.3%; Score 1249.5; DB 9; Length 364;
Best Local Similarity 69.2%; Pred. No. 2.2e-89;
Matches 225; Conservative 50; Mismatches 49; Indels 1; Gaps 1;

```
Qy          4 MKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 63

Db          1 MKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 60

Qy         64 HLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATI 123

Db         61 HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV 120

Qy        124 IKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSS 183

Db        121 VKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEIHSV 180

Qy        184 NAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDH 243

Db        181 TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA 240

Qy        244 LSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSEND 303

Db        241 VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL-NG 299
```

```
Qy        304 YLQDCLDAIQQDFVIFNREKLKRSQ 328
              :|| ||: ::::|:|||||||:| |
Db        300 HLQHCLETVREEFIIFNREKLRRQQ 324


RESULT 4
US-10-195-888-572
; Sequence 572, Application US/10195888
; Publication No. US20060073545A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C324
;  CURRENT APPLICATION NUMBER: US/10/195,888
;  CURRENT FILING DATE:  2002-07-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-195-888-572

  Query Match             64.3%;  Score 1249.5;  DB 9;  Length 364;
  Best Local Similarity   69.2%;  Pred. No. 2.2e-89;
  Matches  225;  Conservative   50;  Mismatches   49;  Indels    1;  Gaps    1;

Qy          4 MKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 63
              |||||||:|||||||||||||||:|:| :|| ||||||||||||||||||||||||||||
Db          1 MKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 60

Qy         64 HLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATI 123
              |||||| |:| ||:|||||:||||:||:  ||||||:||||||||| || |:|||||||:
Db         61 HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV 120

Qy        124 IKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSS 183
              :|  |||:::|||||||||:|  ::: | |||: |||||:|: ||||||||||:|||
Db        121 VKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEIHSV 180

Qy        184 NAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDH 243
                :: :: :|     | |  || | |||||||||| :|| |:||| |:|: | || : ||
Db        181 TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA 240

Qy        244 LSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSEND 303
              : :| : ||||||||||:|||||||||||||:||||||||||:||| ::||    |
Db        241 VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL-NG 299

Qy        304 YLQDCLDAIQQDFVIFNREKLKRSQ 328
              :|| ||: ::::|:|||||||:| |
Db        300 HLQHCLETVREEFIIFNREKLRRQQ 324


RESULT 5
US-10-195-889-572
; Sequence 572, Application US/10195889
; Publication No. US20060074227A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C329
;  CURRENT APPLICATION NUMBER: US/10/195,889
;  CURRENT FILING DATE:  2002-07-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-195-889-572

  Query Match             64.3%;  Score 1249.5;  DB 9;  Length 364;
  Best Local Similarity   69.2%;  Pred. No. 2.2e-89;
  Matches  225;  Conservative   50;  Mismatches   49;  Indels    1;  Gaps    1;

Qy          4 MKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 63
              |||||||:|||||||||||||||:|:| :|| ||||||||||||||||||||||||||||
Db          1 MKYMNKQKCIERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY 60

Qy         64 HLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATI 123
              |||||| |:| ||:|||||:||||:||:  ||||||:||||||||| || |:|||||||:
Db         61 HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV 120

Qy        124 IKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSS 183
              :|  |||:::|||||||||:|  ::: | |||: |||||:|: ||||||||||:|||
Db        121 VKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEIHSV 180

Qy        184 NAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDH 243
                :: :: :|     | |  || | |||||||||| :|| |:||| |:|: | || : ||
Db        181 TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA 240

Qy        244 LSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSEND 303
              : :| : ||||||||||:|||||||||||||:||||||||||:||| ::||    |
Db        241 VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPL-NG 299

Qy        304 YLQDCLDAIQQDFVIFNREKLKRSQ 328
              :|| ||: ::::|:|||||||:| |
Db        300 HLQHCLETVREEFIIFNREKLRRQQ 324


RESULT 6
US-11-125-295-11
; Sequence 11, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/11/125,295
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US/10/620,845
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-125-295-11

  Query Match            59.0%;  Score 1146.5;  DB 11;  Length 396;
  Best Local Similarity   63.1%;  Pred. No. 2.3e-81;
  Matches  219;  Conservative   47;  Mismatches   72;  Indels    9;  Gaps    3;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||:|:||:||||||:||:|:| :|| |||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||| | |:||:|:|||: :|||||: | |||||:|||||||| || |:|||||
Db        108 LRYHLQQNVHFKEETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              | ::    : | :|||||||||:| |    | |||| |||||:|| ||||||| ||| |
Db        168 AAMLPRETQITTMAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGVTAYELLRGRRPYHI 225

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
               || : : :|  | |  | |   ||:|||:||:|||  ||: | | | |||  | :  :
Db        226 RSSTSSKEIVHTFETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDIN 285

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || : :||: |||:||||||:|||||||||||||:|||||||||| :      ||||:
Db        286 WDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSSQT 345

Qy        301 ENDYLQDCLDAIQQDFVIFNREKL-----KRSQDLPREPLPAPESRD 342
                  ||: ||::|::|:||||||:     ||  :|  |    |:  |
Db        346 --CLLQEHLDSVQKEFIIFNREKVNRDFNKRQPNLALEQTKDPQGED 390


RESULT 7
US-11-125-295-9
; Sequence 9, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/11/125,295
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US/10/620,845
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 407
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-125-295-9

  Query Match            58.8%;  Score 1142;  DB 11;  Length 407;
  Best Local Similarity   63.2%;  Pred. No. 5.4e-81;
  Matches  216;  Conservative   50;  Mismatches   72;  Indels    4;  Gaps    2;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||:|:||:||||||:||:|:| :|| |||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||| | |:||:|:|||: :|||||: | |||||:|||||||| || |:|||||
Db        108 LRYHLQQNVHFKEETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              | ::    : | :|||||||||:| |    | |||| |||||:|| ||||||| ||| |
Db        168 AAMLPRETQITTMAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGVTAYELLRGRRPYHI 225

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVL 240
               || : : :|  | |  | |   ||:|||:||:|||  ||: | | | |||  | :  :
Db        226 RSSTSSKEIVHTFETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDIN 285

Qy        241 WDHLSEKRVEPGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
              || : :||: |||:||||||:|||||||||||||:|||||||||| :      ||||:
Db        286 WDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSSQT 345

Qy        301 ENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPESRD 342
                  ||: ||::|::|:||||||: |  :  :  |   :::|
Db        346 --CLLQEHLDSVQKEFIIFNREKVNRDFNKRQPNLALEQTKD 385


RESULT 8
US-11-125-295-5
; Sequence 5, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/11/125,295
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US/10/620,845
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-125-295-5

  Query Match            36.5%;  Score 709;  DB 11;  Length 225;
  Best Local Similarity   74.1%;  Pred. No. 8.8e-48;
  Matches  129;  Conservative   21;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||:|:||:||||||:||:|:| :|| |||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |||||||| | |:||:|:|||: :|||||: | |||||:|||||||| || |:|||||
Db        108 LRYHLQQNVHFKEETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRG 174
              | ::    : | :|||||||||:| |    | |||| |||||:|| |||||||
Db        168 AAMLPRETQITTMAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGVTAYELLRG 219


RESULT 9
US-11-125-295-7
```

```
; Sequence 7, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Nepomnichy, Boris
;  APPLICANT:  Wang, Xiaoming
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Scoville, John
;  APPLICANT:  Walke, D. Wade
;  TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0167-USA
;  CURRENT APPLICATION NUMBER: US/11/125,295
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US/10/620,845
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/841,683
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,499
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 60/201,227
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-125-295-7

  Query Match             36.5%;  Score 709;  DB 11;  Length 236;
  Best Local Similarity   74.1%;  Pred. No. 9.3e-48;
  Matches  129;  Conservative   21;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              ||||||||||:|:||:||||||:||:|:| :|| ||||||||||||||||||||||||||
Db         48 MYAMKYMNKQKCVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              ||||||||| | |:||:|:|||: :|||||: | |||||:||||||||| || |:|||||
Db        108 LRYHLQQNVHFKEETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNI 167

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRG 174
              | ::    : | :||||||||||:| |    | |||| |||||:|| |||||||
Db        168 AAMLPRETQITTMAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGVTAYELLRG 219


RESULT 10
US-10-505-928-349
; Sequence 349, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 349
;   LENGTH: 733
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-505-928-349

  Query Match             23.6%;  Score 458;  DB 8;  Length 733;
  Best Local Similarity   37.5%;  Pred. No. 1.1e-27;
  Matches  103;  Conservative   51;  Mismatches  103;  Indels   18;  Gaps    6;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| : |     || ||:   | :|| |: | |:| | |:|| |  :::::| | |||
Db         87 LYAMKVLKKATLKVRDRVRSKM-ERDILAEVNHPFIVKLHYAFQTEGKLYLILDFLRGGD 145

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |   | : | |:|: |: |: |:|||||:|    ||:||:||:|||||| ||  :||| :
Db        146 LFTRLSKEVMFTEEDVKFYLAELALALDHLHSLGIIYRDLKPENILLDEEGHIKITDFGL 205

Qy        121 A-TIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              :  |   :|| :  ||  |||||: :       |::   |||| ||: :|:| |  |:
Db        206 SKEAIDHDKRAYSFCGTIEYMAPEVVNR-----RGHTQSADWWSFGVLMFEMLTGSLPFQ 260

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSS----LQDVQAAPA 235
                  :|:       |::   | |  :||| |   || :|| :    :::::  |
Db        261 GKDRKETMALILKAKLGMPQFL---SGEAQSLLRALFKRNPCNRLGAGIDGVEEIKRHPF 317

Qy        236 LAGVLWDHLSEKRVEPGFVPNKGR----LHCDPTF 266
                : |: |  | ::| | |  ||     | || |
Db        318 FVTIDWNTLYRKEIKPPFKPAVGRPEDTFHFDPEF 352


RESULT 11
US-10-878-556A-129
; Sequence 129, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
;  APPLICANT: Hoffmann La-Roche Inc.
;  TITLE OF INVENTION: HCV regulated protein expression
;  FILE REFERENCE: 21762
;  CURRENT APPLICATION NUMBER: US/10/878,556A
;  CURRENT FILING DATE:  2004-06-28
;  NUMBER OF SEQ ID NOS: 199
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
;   LENGTH: 740
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: sw_hum/k6a3_human
;   DATABASE ENTRY DATE: 1996-10-01
US-10-878-556A-129

  Query Match             22.9%;  Score 444;  DB 9;  Length 740;
  Best Local Similarity   36.4%;  Pred. No. 1.4e-26;
  Matches  100;  Conservative   52;  Mismatches  105;  Indels   18;  Gaps    6;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| : |     || ||    | :|| |: | |:| | |:|| |  :::::| | |||
Db         96 LYAMKVLKKATLKVRDRVRTKM-ERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGD 154

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              |   | : | |:|: |: |: |:|||||:|    ||:||:||:|||||| ||  |||| :
Db        155 LFTRLSKEVMFTEEDVKFYLAELALALDHLHSLGIIYRDLKPENILLDEEGHIKLTDFGL 214

Qy        121 ATIIKDGE-RATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYD 179
              :    | | :| :  ||  |||||: :       |::   |||| ||: :|:| |  |:
Db        215 SKESIDHEKKAYSFCGTVEYMAPEVVNR-----RGHTQSADWWSFGVLMFEMLTGTLPFQ 269

Qy        180 IHSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSS----LQDVQAAPA 235
                    :::       |::   | |  :||| |   || :|| :    :::::
Db        270 GKDRKETMTMILKAKLGMPQFL---SPEAQSLLRMLFKRNPANRLGAGPDGVEEIKRHSF 326

Qy        236 LAGVLWDHLSEKRVEPGFVPNKGR----LHCDPTF 266
                : : |: |  : : | | |  ||     : || |
Db        327 FSTIDWNKLYRREIHPPFKPATGRPEDTFYFDPEF 361


RESULT 12
US-11-188-298-19312
; Sequence 19312, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53452)B
;  CURRENT APPLICATION NUMBER: US/11/188,298
```

```
;  CURRENT FILING DATE:  2005-07-22
;  PRIOR APPLICATION NUMBER: 60/592,978
;  PRIOR FILING DATE: 2004-07-31
;  NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19312
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-11-188-298-19312

  Query Match             22.4%;  Score 435.5;  DB 11;  Length 502;
  Best Local Similarity   35.2%;  Pred. No. 3.8e-26;
  Matches   92;  Conservative   56;  Mismatches   94;  Indels   19;  Gaps    5;

Qy          2 YAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDL 61
              ||:| : | | ::  :| :   |  :|  : | ||: || ::||  :::||:| : ||:|
Db        217 YAIKVLKKAQVVKMKQVEHTNDERRMLNRVRHPFLITLWGTWQDARNLYMVMDFVEGGEL 276

Qy         62 RYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIA 121
                 |::: :|    : |  |: |||:||  | ||:||:||:|:|||  ||  :|||  |
Db        277 FSLLRKSQRFPNPVAKFYAAEVTLALEYLHSQQIIYRDLKPENLLLDRHGHLKITDFGFA 336

Qy        122 TIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIH 181
               : |       | ||  |:|||:  |       ||:  |||||:|:: :|:| |: |:
Db        337 KEVPD--ITWTLCGTPDYLAPEVVSS-----KGYNKSVDWWSLGILIFEMLCGFTPFWDS 389

Qy        182 SSNAVESLVQLFSTV---SVQYVPTWSKEMVALLRKLLTVNPEHRLSSL----QDVQAAP 234
              |      |:::  :    |:| |    : | || :|:|  :   || :|    :||:  |
Db        390 GSP-----VKIYENILRGRVKYPPYLHPDAVDLLSQLITADLTKRLGNLHGGSEDVKNHP 444

Qy        235 ALAGVLWDHLSEKRVEPGFVP 255
              | | || |: | ::  :||
Db        445 WFAEVTWDRLARKDIDAPYVP 465


RESULT 13
US-11-096-568A-31309
; Sequence 31309, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31309
;   LENGTH: 385
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(385)
;   OTHER INFORMATION: Ceres Seq. ID no. 13579400
US-11-096-568A-31309

  Query Match             22.4%;  Score 435;  DB 11;  Length 385;
  Best Local Similarity   32.1%;  Pred. No. 3e-26;
  Matches  101;  Conservative   55;  Mismatches  123;  Indels   36;  Gaps    6;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| | | : :|::    :  | :|| :|:| |:| | |||| :  :::|:| : ||
Db         79 IYAMKVMRKDKIVEKNHAEYMKAERDILTKIDHPFIVQLKYSFQTKYRLYLVLDFINGGH 138

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              | : |     | ||  |:|  |:  |: :|  : |:|||:||:|||:|  ||  |||| :
Db        139 LFFQLYHQGLFREDLARVYTAEIVSAVSHLHEKGIMHRDLKPENILMDVDGHVMLTDFGL 198

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |   ::  |: :: ||  ||||||       | |:    ||||||:: ||:| |  |: :
Db        199 AKEFEENTRSNSMCGTTEYMAPEIVR-----GKGHDKAADWWSVGILLYEMLTGKPPF-L 252

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRL----SSLQDVQAAPAL 236
              |   ::  :         |::   | |  |||: ||   || ||    |  ::::
Db        253 GSKGKIQQKIVKDKIKLPQFL---SNEAHALLKGLLQKEPERRLGSGPSGAEEIKKHKWF 309

Qy        237 AGVLWDHLSEKRVEPGFVPNKGRLHCDPTFE---LEEMILES----------------- 275
              : |  |  : |:| | |       |   |:    :  :|:|
Db        310 KAINWKKLEAREVQPSFKPAVSGRQCIANFDKCWTDMSVLDSPASSPNSDAKANPFTNFT 369

Qy        276 --RPLHKKKKRLAKN 288
                || |    |  |
Db        370 YVRPPHSFLHRTTSN 384


RESULT 14
US-11-096-568A-31308
; Sequence 31308, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31308
;   LENGTH: 424
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(424)
;   OTHER INFORMATION: Ceres Seq. ID no. 13579399
US-11-096-568A-31308

  Query Match             22.4%;  Score 435;  DB 11;  Length 424;
  Best Local Similarity   32.1%;  Pred. No. 3.4e-26;
  Matches  101;  Conservative   55;  Mismatches  123;  Indels   36;  Gaps    6;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| | | : :|::    :  | :|| :|:| |:| | |||| :  :::|:| : ||
Db        118 IYAMKVMRKDKIVEKNHAEYMKAERDILTKIDHPFIVQLKYSFQTKYRLYLVLDFINGGH 177

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              | : |     | ||  |:|  |:  |: :|  : |:|||:||:|||:|  ||  |||| :
Db        178 LFFQLYHQGLFREDLARVYTAEIVSAVSHLHEKGIMHRDLKPENILMDVDGHVMLTDFGL 237

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |   ::  |: :: ||  ||||||       | |:    ||||||:: ||:| |  |: :
Db        238 AKEFEENTRSNSMCGTTEYMAPEIVR-----GKGHDKAADWWSVGILLYEMLTGKPPF-L 291

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRL----SSLQDVQAAPAL 236
              |   ::  :         |::   | |  |||: ||   || ||    |  ::::
Db        292 GSKGKIQQKIVKDKIKLPQFL---SNEAHALLKGLLQKEPERRLGSGPSGAEEIKKHKWF 348

Qy        237 AGVLWDHLSEKRVEPGFVPNKGRLHCDPTFE---LEEMILES----------------- 275
              : |  |  : |:| | |       |   |:    :  :|:|
Db        349 KAINWKKLEAREVQPSFKPAVSGRQCIANFDKCWTDMSVLDSPASSPNSDAKANPFTNFT 408

Qy        276 --RPLHKKKKRLAKN 288
                || |    |  |
Db        409 YVRPPHSFLHRTTSN 423


RESULT 15
US-11-096-568A-31307
; Sequence 31307, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
```

```
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31307
;   LENGTH: 471
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(471)
;   OTHER INFORMATION: Ceres Seq. ID no. 13579398
US-11-096-568A-31307

  Query Match             22.4%;  Score 435;  DB 11;  Length 471;
  Best Local Similarity   32.1%;  Pred. No. 3.9e-26;
  Matches  101;  Conservative   55;  Mismatches  123;  Indels   36;  Gaps    6;

Qy          1 MYAMKYMNKQQCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD 60
              :|||| | | : :|::    :  | :|| :|:| |:| | |||| :  :::|:| : ||
Db        165 IYAMKVMRKDKIVEKNHAEYMKAERDILTKIDHPFIVQLKYSFQTKYRLYLVLDFINGGH 224

Qy         61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
              | : |      | ||  |:|  |:  |: :|  : |:|||:||:|||:|  ||  |||| :
Db        225 LFFQLYHQGLFREDLARVYTAEIVSAVSHLHEKGIMHRDLKPENILMDVDGHVMLTDFGL 284

Qy        121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
              |   ::  |: :: ||  ||||||       | |:    ||||||:: ||:| |  |: :
Db        285 AKEFEENTRSNSMCGTTEYMAPEIVR-----GKGHDKAADWWSVGILLYEMLTGKPPF-L 338

Qy        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRL----SSLQDVQAAPAL 236
              |   ::  :        |::   | |  |||: ||   || ||    |  ::::
Db        339 GSKGKIQQKIVKDKIKLPQFL---SNEAHALLKGLLQKEPERRLGSGPSGAEEIKKHKWF 395

Qy        237 AGVLWDHLSEKRVEPGFVPNKGRLHCDPTFE---LEEMILES----------------- 275
              : |  |  : |:| | |       |   |:    :  :|:|
Db        396 KAINWKKLEAREVQPSFKPAVSGRQCIANFDKCWTDMSVLDSPASSPNSDAKANPFTNFT 455

Qy        276 --RPLHKKKKRLAKN 288
                || |    |   |
Db        456 YVRPPHSFLHRTTSN 470


Search completed: May  9, 2006, 10:50:03
Job time : 18 secs
```

THIS PAGE LEFT BLANK